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U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

TSRI 615.1

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

09/622500

INTERNATIONAL APPLICATION NO.
PCT/US99/04716INTERNATIONAL FILING DATE
3 March 1999PRIORITY DATE CLAIMED
3 March 1998TITLE OF INVENTION RESISTANCE IN PLANTS TO INFECTION BY ssDNA VIRUS USING
INOVIRIDAE VIRUS ssDNA-BINDING PROTEIN, COMPOSITIONS AND METHODS OF USE

APPLICANT(S) FOR DO/EO/US

Padidam, et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☒ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). - copy
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☐ A FIRST preliminary amendment.
☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:
 - Return Receipt Postcard
 - Certificate of Express Mailing

17. ☒ The following fees are submitted:**BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :**

Neither international preliminary examination fee (37 CFR 1.482)
nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO
and International Search Report not prepared by the EPO or JPO \$970.00

International preliminary examination fee (37 CFR 1.482) not paid to
USPTO but International Search Report prepared by the EPO or JPO \$840.00

International preliminary examination fee (37 CFR 1.482) not paid to USPTO but
international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$690.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)
but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$670.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)
and all claims satisfied provisions of PCT Article 33(1)-(4) \$96.00

ENTER APPROPRIATE BASIC FEE AMOUNT =**CALCULATIONS** PTO USE ONLY

\$ 670.00

Surcharge of \$130.00 for furnishing the oath or declaration later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(e)).

\$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE
Total claims	50 - 20 =	30	X \$18.00
Independent claims	4 - 3 =	1	X \$78.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$260.00

\$ 540.00

\$ 78.00

\$

TOTAL OF ABOVE CALCULATIONS =

\$ 1,288.00

Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement
must also be filed (Note 37 CFR 1.9, 1.27, 1.28).

\$

SUBTOTAL =

\$ 1,288.00

Processing fee of \$130.00 for furnishing the English translation later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

TOTAL NATIONAL FEE =

\$ 1,288.00

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +

\$

TOTAL FEES ENCLOSED =

\$ 1,288.00

Amount to be
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\$

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\$

a. ☒ A check in the amount of \$ 1,288.00 to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees.
A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any
overpayment to Deposit Account No. 19-0962. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

THE SCRIPPS RESEARCH INSTITUTE
Office of Patent Counsel
10550 North Torrey Pines Road, TPC-8
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SIGNATURE:

Thomas Fitting

NAME

34,163

REGISTRATION NUMBER

RESISTANCE IN PLANTS TO INFECTION BY ssDNA VIRUS
USING INOVIRIDAE VIRUS ssDNA-BINDING PROTEIN,
COMPOSITIONS AND METHODS OF USE

Technical Field

The invention relates methods and compositions for producing plants which are resistant to infection by plant viruses.

Background

Geminiviruses are plant pathogens that cause significant yield losses in crop plants in many countries of the world (Briddon et al, "Geminiviridae", p. 158-165. In F. A. Murphy (ed.), Virus Taxonomy. Sixth Report of International Committee on Taxonomy of Viruses. Springer-Verlag, Vienna & New York, 1995; Frischmuth et al, Semin. Virol., 4:329-337, 1993; Harrison et al, Ann. Rev. Phytopathol., 23:55-82, 1985; Polston et al, Plant Dis., 81:1358-1369, 1997). Different members are transmitted by whiteflies or leafhoppers (Davies et al, Genet., 5:77-81, 1989; Lazarowitz et al, Crit. Rev. Plant Sci., 11:327-349, 1992). Most of the whitefly-transmitted geminiviruses (WTGs) have bipartite genomes while all the leafhopper-transmitted geminiviruses and some of the WTGs have monopartite genomes. The monopartite genomes (2566-3028 nt) encode proteins required for replication, encapsidation and movement, while in the case of the bipartite viruses the movement functions are encoded by a second genome component of similar size (Davies et al, Genet., 5:77-81, 1989; Ingham et al, Virology, 207:191-204, 1995; Timmermans et al, Annu. Rev. Plant Physiol. Plant Mol. Biol., 45:79-112, 1994).

Geminiviruses have circular single-stranded (ss) DNA genomes encapsidated in double icosahedral particles. Geminiviruses replicate via a rolling circle mechanism analogous

to replication of bacteriophages with ssDNA genomes. The incoming geminivirus single-stranded (ss) DNA is converted by host enzymes to double-stranded (ds) DNA which in turn serves as a template for transcription of early, replication associated genes on the complementary-sense strand. Replication initiator protein (Rep or AC1) is the only viral protein required for replication. In bipartite geminiviruses, a second protein (AC3) enhances replication. AC2, another early gene product, transactivates expression of the coat protein (CP) gene on the virion-sense strand. While the CP is not required for replication of the virus in protoplasts or plants, mutations in CP lead to dramatic decreases in accumulation of ssDNA in protoplasts or plants without affecting the accumulation of dsDNA. On the other hand, tomato golden mosaic virus CP mutations had no effect on DNA accumulation in plants, but reduced ssDNA accumulation while increasing the dsDNA accumulation in protoplasts. In plants, lack of CP results in a complete loss of infectivity of monopartite viruses but not bipartite viruses.

Coat protein may influence the ratios of ss and dsDNA levels in a passive manner by depleting the ssDNA that is available for conversion to dsDNA through encapsidation, or by modulating ssDNA synthesis, or both. No evidence is available for how CP influences ssDNA accumulation in geminiviruses. In tomato leaf curl virus from New Delhi (ToLCV-NbE, hereafter referred as ToLCV), a geminivirus with bipartite genome, disrupting the synthesis of wild type CP resulted in drastic reduction in ssDNA and a three to five fold increase in dsDNA accumulation in infected protoplasts. Inoculated plants, however, develop severe symptoms and accumulate wild type levels of dsDNA and low levels of ssDNA.

There remains a need to better understand the role of CP in

geminivirus replication.

Brief Summary of the Invention

We have now discovered that a heterologous ssDNA binding
5 protein can complement CP function in geminivirus ssDNA
accumulation. It is also discovered that ToLCV modified to
express the ssDNA binding gene 5 protein (g5p) from E. coli
phage M13 in place of CP accumulates ssDNA to wild type levels
in protoplasts, but fails to move efficiently in plants,
10 providing key insight into the present invention. Exemplary
heterologous ssDNA-binding proteins are found in the Inoviridae
virus family.

Thus, in one embodiment, the invention describes a method
for producing in a plant resistance to a single stranded DNA
15 (ssDNA) virus comprising introducing a ssDNA-binding protein of
the Inoviridae virus family into the plant. The Inoviridae
family virus ssDNA-binding protein
is selected from the group consisting of the Inovirus and
Plectrovirus genuses, and the Inovirus genus virus is selected
20 from the group consisting of Coliphage, enterobacteria phage,
Pseudomonas phage, Vibrio phage and Xanthomonas phage species.
A preferred Coliphage species of virus is selected from the
group consisting of AE2, dA, Ec9, f1, fd, HR, M13, ZG/2 and ZJ/2
coliphages, with a coat protein or a gene 5 protein being more
25 preferred. Particularly preferred is the Coliphage M13 gene 5
protein.

The method of introduction of the ssDNA-binding protein
into the plant can include producing a transgenic plant
containing an expression vector for expressing the protein,
30 contacting a plant with an expression vector for expressing the
protein, infecting the plant with a carrier vector, such as an
Agrobacterium vector, and the like methods.

The invention also describes a DNA expression vector comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family, wherein the vector is capable of expressing the protein in plants. The vector is used
5 in the methods described herein.

Also described is a composition for producing resistance to a ssDNA virus that infects plants comprising an effective amount of a DNA expression vector comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family,
10 wherein the vector is capable of expressing the protein in the plant. In preferred embodiments, the vector is a carrier vector which can infect the plant. A particularly preferred vector is an Agrobacterium vector.

The invention also contemplates a transgenic plant
15 containing a DNA expression vector of this invention, which is resistant to ssDNA virus infection due to the expression of a ssDNA binding protein as described herein.

Other embodiments will be apparent from the teachings of the specification and the claims.

Brief Description of the Drawings

Figure 1 illustrates the genome organization and schematic representation of constructs of tomato leaf curl virus from New Delhi (ToLCV-Nde). Figure 1A illustrates the genome organization
25 of ToLCV-Nde showing the ORFs and their functions. CR, common region for both components. Figure 1B illustrates a linear physical map of AV2 and CP region of ToLCV-Nde is shown at the bottom with nucleotide positions and relevant restriction enzyme sites. The positions of different gene replacements are shown
30 above the linear map. Note that the gene replacements shown are not to the scale. Descriptions of the constructs are given in Table 1.

Figure 2 illustrates replication of ToLCV constructs in infected BY2 protoplasts. Southern blot analysis was performed as described in the Examples. The viral constructs used for infecting protoplasts are shown above the lanes. Protoplasts were inoculated with A component DNA alone (lanes 1-11) or coinoculated with A and B component DNAs (lanes 12-15). Each lane contained 4 μ g of DNA prepared from protoplasts (single transfection). Viral DNA was detected using a radioactively-labeled probe from A component DNA. The position of supercoiled (sc), single-stranded (ss), open circular (op), and linear (li) viral DNA forms are indicated. Note that the positions of supercoiled and other viral DNA forms in lane 11 are shifted upwards due to larger size of the CP66:6G:BC1 construct.

Figure 3 illustrates indirect immunofluorescence of proteins expressed in protoplasts (Figures 3A-3G) and fluorescence of green fluorescent protein (GFP) expressed in plants (Figures 3H-3P). Protoplasts were transfected and antigens were visualized with different antibodies and FITC- or rhodamine-conjugated secondary antibody. GFP fluorescence in plants was monitored every three days for 15 days and the area shown corresponds to 2.5 X 2.5 mm of leaf area. (Figure 3A) Protoplast infected with CP66:Stag:6G:g5 virus and stained with S-protein coupled to FITC. (Figure 3B) Protoplast infected with wild type virus and stained with anti-CP antisera. (Figure 3C) Protoplast infected with CP66:GUS virus and stained with anti-GUS antisera. (Figure 3D) Protoplast infected with g5:GUSAV2-CP virus and stained with anti-GUS antisera. (figure 3E) Protoplast infected with GUSAV2-CP virus and stained with anti-GUS antisera. (Figure 3F) Protoplast infected with FBV1AV2-CP virus and stained with anti-Flag antibody. (Figure 3G) Protoplasts infected with TBC1AV2-CP virus and stained with anti-T7 tag antibody. Note that two cells are shown in this micrograph.

Inoculated leaf (Figure 3H) and systemic leaf (Figure 3I) of a plant infected with GFPNAV2-CP + CP66:g5 viruses 6 days post inoculation (dpi). Inoculated leaf (Figure 3J) and systemic leaf (Figure 3K) of a plant infected with GFPNAV2-CP + CP66:g5 viruses 15 dpi. Inoculated leaf (Figure 3L) and systemic leaf (Figure 3M) of a plant infected with GFPNAV2-CP + CP66:6G:g5 viruses 6 dpi. Inoculated leaf (Figure 3N) and systemic leaves (Figures 3O and 3P) of a plant infected with GFPNAV2-CP + CP66:6G:g5 viruses 15 dpi.

Figure 4 illustrates in vivo binding of gene 5 protein to ToLCV-Nde DNA. (Figure 4A) Flag epitope-tagged CP66:6G:g5 protein expressed in protoplasts was immunoprecipitated with anti-Flag antibody coupled to agarose after lysing protoplasts in NP40 buffer containing different concentrations of NaCl (shown above the lanes) or RIPA buffer, and the immunoprecipitated protein was detected on a western blot with anti-Flag antibody (lanes 2-6). Lane 1 contained proteins immunoprecipitated from protoplasts transfected with wild type virus as a control. The protein band present in all lanes at ~24 kDa is the light chain of anti-Flag antibody used for immunoprecipitations. The immunoprecipitated CP66:6G:g5 protein was detected at two different molecular masses corresponding to monomer and dimer forms. Positions of molecular weight markers are indicated in kilodaltons on the left. (Figure 4B) Viral ssDNA that coimmunoprecipitated with the Flag epitope-tagged CP66:6G:g5 protein was detected on a Southern blot using ³²P-labeled A component DNA as a probe. Lanes 1-7 have same treatments as shown in Figure 4A.

Detailed Description of the Invention

The invention is based on the discovery that ssDNA-binding protein of the Inoviridae family of viruses interferes with

virus spread during the infection process of plant viruses of the ssDNA type. By inhibiting virus spread, the virus infection is reduced and/or blocked, thereby increasing plant "resistance" to the virus infection.

5 The invention describes methods for inhibiting ssDNA plant viruses using Inoviridae family virus ssDNA binding protein, expression vectors capable of expressing the binding protein in plants, compositions for delivery of the expression vectors, and transgenic plants containing genes capable of expressing the
10 binding protein.

A. Methods for Inhibiting ssDNA Plant Viruses

 The invention contemplates methods for producing in a plant resistance to infection and/or virulence of a single
15 stranded DNA (ssDNA) virus. The method comprises introducing a ssDNA-binding protein from the *Inoviridae* family virus into a susceptible plant.

 The ssDNA-binding protein is typically provided by expression of a nucleotide sequence which encodes the ssDNA-
20 binding protein and which contains expression control elements which provide for expression of protein in plants.

 Introduction of the protein into the plant can be accomplished by a variety of methods including standard gene transfer methods, inoculation of the plant with a transfer or
25 carrier vector (i.e., infection by an engineered plant virus or phage), "biolistic" (i.e., ballistic) introduction of nucleic acids into mature plant tissue, direct DNA uptake into plant protoplast, transformation of plants with *Agrobacterium tumefaciens*-based vectors, and the like well known methods.

30 Plant expression elements for a nucleotide sequence are generally well known in the art and are not to be considered limiting to the invention. The nucleotide sequence which

encodes the ssDNA-binding protein can be present on an expression vector, as a DNA fragment, or as a component of a "transfer" or carrier vector such as the infectious *Agrobacterium* gene transfer system commonly used in plants.

5 A preferred ssDNA-binding protein is an *Inoviridae* family virus protein having the ability to bind ssDNA. The preferred protein is either the viral coat protein or the viral "gene 5" protein. Although whole (i.e., native) protein can be used, portions of the whole protein can also be used that contain the
10 ssDNA binding portion of the protein. In addition, it is understood that modifications to the amino acid residue sequence of a native protein can be made without compromising the essential functional properties of the protein according to the invention. Thus, the term "ssDNA-binding protein" means any of
15 a variety of configuration of protein including active fragments, fusion proteins containing an active fragment, whole protein, and derivatives thereof which possess the ssDNA binding activity.

The ability to bind ssDNA can be readily measured by art-
20 recognized procedures, including the binding methods described herein. Thus, the invention is not to be construed as so limited so long as the ssDNA-binding protein has the ability to bind plant viral ssDNA as described herein, and inhibit virus replication and/or viral pathogenesis.

25 The *Inoviridae* family of viruses is a large family that includes the *Inovirus* and *Plectrovirus* genera. Preferred *Inovirus* species include Coliphage, enterobacteria phage, *Pseudomonas* phage, *Vibrio* phage and *Xanthomonas* phage species. Preferred Coliphage species include AE2, dA, Ec9, f1, fd, HR,
30 M13, ZG/2 and ZJ/2 coliphages. A particularly preferred protein is the Coliphage M13 gene 5 protein.

In preferred embodiments, the Coliphage M13 gene 5 protein

has the amino acid residue sequence shown in SEQ ID NO 1.

In a related embodiment, the method comprises introducing the ssDNA-binding protein by preparing a transgenic plant which comprises a gene capable of expressing the protein, and thereby
5 providing plant resistance to the ssDNA plant virus. The methods for preparing a transgenic plant capable of expressing an foreign protein such as the ssDNA-binding protein of this invention are described further herein.

In a further related embodiment, the methods comprises
10 introducing the ssDNA-binding protein by contacting the plant with a composition containing an expression vector capable of expressing the protein in the plant. Methods for preparing and using an expression vector in a composition according to the invention are described further herein.

15 In the various nucleic acid-based methods in which a nucleotide sequence encodes the ssDNA-binding protein and is capable of expressing the protein, it is understood that the nucleotide sequence can vary in content so long a contemplated ssDNA-binding protein is encoded. For example, the genetic code
20 tolerates variation in codon usage for encoding an amino acid residue sequence, and therefore the invention is not to be construed as limited to a particular nucleotide sequence. However, it is also understood that an expression environment, e.g., the plant cell, has codon usage preferences, and therefore
25 it is desirable to utilize the preferred codons to optimize expression of expressible genes in plants.

In this regard, a preferred nucleotide sequence for use in an expression vector or transgenic plant of this invention can utilize preferred codons. A particularly preferred nucleotide
30 sequence for use in the present invention encodes an M13 gene 5 protein, preferably the amino acid residue sequence shown in SEQ ID NO 1. In one embodiment, a preferred nucleotide sequence

comprises the nucleotide sequence shown in SEQ ID NO 2 which is the native nucleotide sequence from the M13 viral genome encoding the native M13 gene 5 protein. In another embodiment, a preferred nucleotide sequence comprises the nucleotide

5 sequence shown in SEQ ID NO 3 which is a synthetic nucleotide sequence designed to incorporate preferred codon usages for highly expressed human genes, and which encodes the native M13 gene 5 protein.

The complete sequence of bacteriophage M13, including the
10 gene 5 coding sequence, is available from GenBank as Accession numbers V00604, J02461 and M10377. The amino acid residue sequence and nucleotide sequence encoding M13 gene 5 is shown in SEQ ID Nos 1 and 2, respectively.

The introduced protein is effective at inhibiting infection
15 of any ssDNA virus that infects plants. Preferred viruses are the *Geminiviridae* family of viruses, which includes *Mastrevirus*, *Curtovirus* and *Begomovirus* genera.

Preferred *Mastrevirus* genus species are selected from the group consisting of Bajra streak virus, Bean yellow dwarf virus, Bromus striate mosaic virus, Chickpea chlorotic dwarf virus, Chloris striate mosaic virus, Digitaria streak virus, Digitaria striate mosaic virus, Maize streak virus//Ethiopia, Maize streak virus//Ghana1, Maize streak virus//Ghana2, Maize streak virus//Kenya, Maize streak virus//Komatipoort, Maize streak virus//Malawi, Maize streak virus//Mauritius, Maize streak virus//Mozambique, Maize streak virus//Nigeria1, Maize streak virus//Nigeria2, Maize streak virus//Nigeria3, Maize streak virus//Port Elizabeth, Maize streak virus//Reunion1, Maize streak virus//Reunion2, Maize streak virus//Setaria, Maize streak virus//South Africa, Maize streak virus//Tas, Maize streak virus//Uganda, Maize streak virus//Vaalhart maize, Maize streak virus//Vaalhart wheat, Maize streak

virus//Wheat-eleusian, Maize streak virus//Zaire, Maize streak virus//Zimbabwe1, Maize streak virus//Zimbabwe2, Miscanthus streak virus, Panicum streak virus/Karino, Panicum streak virus/Kenya, Paspalum striate mosaic virus, Sugarcane streak virus//Egypt, Sugarcane streak virus/Natal, Sugarcane streak virus/Mauritius, Tobacco yellow dwarf virus, Wheat dwarf virus/Czech Republic [Wheat dwarf virus-CJI, WDV-CJI], Wheat dwarf virus/France and Wheat dwarf virus/Sweden.

Preferred *Curtovirus* genus species are selected from the group consisting of Beet curly top virus-California, Beet curly top virus-California//Logan, Beet curly top virus-CFH, Beet curly top virus//Iran, Beet curly top virus-Worland, Horseradish curly top virus, Tomato leafroll virus and Tomato pseudo-curly top virus.

Preferred *Begomovirus* genus species are selected from the group consisting of Abutilon mosaic virus, Acalypha yellow mosaic virus, African cassava mosaic virus//Ghana, African cassava mosaic virus/Kenya, African cassava mosaic virus/Nigeria, African cassava mosaic virus/Uganda, Ageratum yellow vein virus, Althea rosea enation virus, Asystasia golden mosaic virus, Bean calico mosaic virus, Bean dwarf mosaic virus, Bean golden mosaic virus-Brazil, Bean golden mosaic virus-Puerto Rico, Bean golden mosaic virus-Puerto Rico/Dominican Rep. [Bean golden mosaic virus-Dominican Rep., BGMV-DR], Bean golden mosaic virus-Puerto Rico/Guatemala [Bean golden mosaic virus-Guatemala, BGMV-GA], Bhendi yellow vein mosaic virus, Chino del tomate virus [Tomato leaf crumple virus, TLCrV], Cotton leaf crumple virus, Cotton leaf curl virus-India, Cotton leaf curl virus-Pakistan1/Faisalabad1 [Cotton leaf curl virus-Pakistan2], Cotton leaf curl virus-Pakistan1/Faisalabad2 [Cotton leaf curl virus-Pakistan3], Cotton leaf curl virus-Pakistan1/Multan [Cotton leaf curl virus-Pakistan1], Cotton leaf

curl virus-Pakistan2/Faisalabad [Pakistani cotton leaf curl virus], Cowpea golden mosaic virus, Croton yellow vein mosaic virus//Lucknow, Dolichos yellow mosaic virus, East african cassava mosaic virus/Kenya, East african cassava mosaic virus/Malawi, East african cassava mosaic virus/Tanzania, East african cassava mosaic virus/Uganda//1 [African cassava mosaic virus-Uganda variant], East african cassava mosaic virus/Uganda//2, Eclipta yellow vein virus, Eggplant yellow mosaic virus, Eupatorium yellow vein virus, Euphorbia mosaic virus, Honeysuckle yellow vein mosaic virus, Horsegum yellow mosaic virus, Indian cassava mosaic virus, Jatropha mosaic virus, Leonurus mosaic virus, Limbean golden mosaic virus, Lupin leaf curl virus, Macroptilium golden mosaic virus-Jamaica//2, Macroptilium golden mosaic virus-Jamaica//3, Macrotyloma mosaic virus, Malvaceous chlorosis virus, Melon leaf curl virus, Mungbean yellow mosaic virus, Okra leaf curl virus//Ivory Coast, Okra leaf curl virus//India, Papaya leaf curl virus, Pepper huasteco virus, Pepper golden mosaic virus, [Texas pepper virus], Pepper mild tigrÄ virus, Potato yellow mosaic virus//Guadeloupe, Potato yellow mosaic virus/Trinidad and Tobago, Potato yellow mosaic virus/Venezuela, Pseuderanthemum yellow vein virus, Rhynchosia mosaic virus, Serrano golden mosaic virus, Sida golden mosaic virus/Costa Rica, Sida golden mosaic virus/Honduras, Sida golden mosaic virus/Honduras//Yellow vein, Sida yellow vein virus, Solanum apical leaf curl virus, Soybean crinkle leaf virus, Squash leaf curl virus, Squash leaf curl virus/Extended host, Squash leaf curl virus/Restricted host, Squash leaf curl virus/Los Mochis, Squash leaf curl virus-China, Tomato golden mosaic virus/Common strain, Tomato golden mosaic virus/Yellow vein strain, Tobacco leaf curl virus//India, Tobacco leaf curl virus-China, Tomato leaf curl virus//Solanum species D1, Tomato leaf curl

virus//Solanum species D2, Tomato leaf curl virus-Australia, Tomato leaf curl virus-Bangalore1 [Indian tomato leaf curl virus-BangaloreI], Tomato leaf curl virus-Bangalore2, [Indian tomato leaf curl virus, ItoLCV], Tomato leaf curl

5 virus-Bangalore3 [Indian tomato leaf curl virus- BangaloreII], Tomato leaf curl virus-New Delhi/Severe [Tomato leaf curl virus-India2, ToLCV-IN1], Tomato leaf curl virus-New Delhi/Mild [Tomato leaf curl virus-India2, ToLCV-IN2], Tomato leaf curl virus-New Delhi/Lucknow [Indian tomato leaf curl virus], Tomato

10 leaf curl virus//Senegal, Tomato leaf curl virus-Sinaloa [Sinaloa tomato leaf curl virus, STL CV], Tomato leaf curl virus-Taiwan, Tomato leaf curl virus-Tanzania, Tomato mottle virus, Tomato mottle virus-Taino [Taino tomato mottle virus, TTMoV], Tomato severe leaf curl virus//Guatemala, Tomato severe

15 leaf curl virus//Honduras, Tomato severe leaf curl virus//Nicaragua, Tomato yellow dwarf virus, Tomato yellow leaf curl virus-China, Tomato yellow leaf curl virus-Israel, Tomato yellow leaf curl virus-Israel/Mild, Tomato yellow leaf curl virus-Israel/Egypt, [Tomato yellow leaf curl virus-Egypt,

20 TYLCV-EG], Tomato yellow leaf curl virus-Israel//Cuba, Tomato yellow leaf curl virus-Israel//Jamaica, Tomato yellow leaf curl virus-Israel//Saudi Arabia1, [Tomato yellow leaf curl virus-Northern Saudi Arabia, TYLCV-NSA], Tomato yellow leaf curl virus-Nigeria, Tomato yellow leaf curl virus-

25 Sardinia, Tomato yellow leaf curl, virus-Sardinia/Sicily [Tomato yellow leaf curl virus-Sicily, TYLCV-SY], Tomato yellow leaf curl virus-Sardinia/Spain//1 [Tomato yellow leaf curl virus-Spain, TYLCV-Sp], Tomato yellow leaf curl virus-Sardinia/Spain//2 [Tomato yellow leaf curl virus-Almeria,

30 TYLCV-Almeria], Tomato yellow leaf curl virus-Sardinia/Spain//3 [Tomato yellow leaf curl virus-European strain], Tomato yellow leaf curl virus-Saudi Arabia [Tomato

yellow leaf curl virus-Southern Saudi Arabia, TYLCV-SSA], Tomato
yellow leaf curl virus-Tanzania, Tomato yellow leaf curl
virus-Thailand//1, Tomato yellow leaf curl virus-Thailand//2 ,
Tomato yellow leaf curl virus//Yemen, Tomato yellow mosaic
5 virus-Brazil//1, Tomato yellow mosaic virus-Brazil//2, Tomato
yellow mottle virus, Tomato yellow vein streak virus-Brazil,
Watermelon chlorotic stunt virus, Watermelon curly mottle virus
and Wissadula golden mosaic virus-Jamaica//1.

Other ssDNA plant viruses include Banana bunchy top virus,
10 Coconut foliar decay virus, Fababean necrotic yellows virus,
Milk vetch dwarf virus and Subterranean clover stunt virus.

The above described ssDNA plant viruses which can be
inhibited by the present methods infect a large number of plant
species. Insofar as new plant species can be discovered which
15 are susceptible to infection by a ssDNA plant virus described
according to the present invention, it is to be understood that
the invention is not intended to be so limited to known plants.
Instead, a plant according to the present methods is intended to
be any plant which is susceptible to infection by the described
20 ssDNA plant virus, which susceptibility can be readily
determined by art recognized methods, including the infection
procedures described herein.

The term "plant" includes whole plants, plant organs (e.g.,
leaves, stems, roots, etc.), seeds and plant cells and progeny
25 of same. The class of plants which can be used in the method of
the invention is generally as broad as the class of higher
plants amenable to transformation techniques, including both
monocotyledonous (monocots) and dicotyledonous (dicots) plants.
It includes plants of a variety of ploidy levels, including
30 polyploid, diploid and haploid.

Exemplary plants which are susceptible to infection, and
therefore are targets for the treatment methods and compositions

described herein include, but are not limited to, a plant is selected from the group consisting of Abutilon, Acalypha, apple, Ageratum, Althea rosea, Asystasia, Bajra, banana, barley, beans, beet, Blackgram, Bromus, Cassava, chickpea, Chilllies, Chloris, clover, coconut, coffee, cotton, cowpea, Croton, cucumber, Digitaria, Dolichos, eggplant, Eupatorium, Euphorbia, fababean, honeysuckle, horsegram, Jatropha, Leonurus, limabean, Lupin, Macroptilium, Macrotyloma, maize, melon, millet, mungbean, oat, okra, Panicum, papaya, Paspalum, peanut, pea, pepper, pigeon pea, pineapple, Phaseolus, potato, Pseuderanthemum, pumpkin, Rhynchosia, rice, Serrano, Sida, sorghum, soybean, squash, sugarcane, sugarbeet, sunflower, sweet potato, tea, tomato, tobacco, watermelon, wheat and Wissadula, or any individual plant or combination of plants thereof.

Preferred examples of the methods of the invention are described herein using the M13 gene 5 protein expressed using a recombinant tomato leaf curl virus (ToLCV) vector on tobacco plants and protoplasts. The ToLCV viral genomic nucleotide sequences for both the A and B components of the ToLCV bipartite genome are known, and are available as GenBank Accession numbers U15015 and U15016, respectively, and are shown in SEQ ID NOS 4 and 5, respectively.

B. Nucleic Acid Molecules

The invention also contemplates a nucleic acid molecule, such as a DNA expression vector, useful for expression of a ssDNA-binding protein of this invention in plants. Thus the nucleic acid molecule contains a nucleotide sequence which encodes the ssDNA-binding protein of this invention and further contains elements for regulation and control of gene expression in plants. Exemplary elements for expression in plants are described in United States Patent Nos. 5,188,642, 5,202,422,

5,463,175 and 5,639,947, the disclosures of which are hereby incorporated by reference. In addition, the methods of manipulating nucleic acids and the production of expression vectors for use in plants is generally well known and therefore
5 not to be construed as limiting to the present invention.

Exemplary expression vectors and systems for introduction of a ssDNA-binding protein into plants are described in the Examples.

Thus, in one embodiment, the invention describes a nucleic
10 acid-based expression system comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family, where the expression system is capable of expressing the protein in a plant susceptible to infection by a ssDNA plant virus as described herein.

15 The ssDNA-binding protein can be any protein as described herein and as is preferred in practicing the methods for the invention. Particularly preferred is the M13 gene 5 protein, such as the amino acid residue sequence shown in SEQ ID NO 1.

The expression system can be a vector or a gene, depending
20 upon the contemplated usage. In the case of a transgenic plant, the invention describes a gene comprising a nucleotide sequence which defines an expression cassette, i.e., the necessary elements for expression of a ssDNA-binding protein structural gene including promoters, transcription start signals,
25 translation start signals, the structural protein coding sequence, and translation and transcription stop sequences, as are well known. In the case of a vector or infectious agent used to introduce an expression cassette, the vector or agent comprises additional genetic elements suitable for the vector or
30 infectious agent's function.

For example, the vector may also contain elements which provide for replication, manipulation and the like, such as in

found on plasmids which facilitate bulk preparation of the vector. In the case of infectious agents, which are typically modified plant viruses or plant phage which can infect the plant, the agent may contain additional elements for replication
5 of the agent and assembly into an infectious particle, as are well known.

A preferred expression cassette in a vector, gene or infectious agent according to the invention comprises a nucleotide sequence shown in SEQ ID NOs 2 or 3 as described
10 herein.

For general cloning of nucleic acids, plasmids are used as are well known. A preferred cloning plasmid used herein is the pBluescript II SK vector (Stratagene, La Jolla, CA). The complete nucleotide sequence of the pBluescript plasmid is
15 available in GenBank as Accession number X52330, and is also shown in SEQ ID NO 6.

For plant transformations, a variety of methods, vectors and agents are available, and therefore the invention is not to be construed as so limited. Exemplary methods include plant
20 transformation, comprising direct uptake of an expression cassette nucleic acid(s) into a protoplast followed by plant regeneration to form a plant, electroporation into a protoplast, biolistic delivery of nucleic acid into either cultured plant cells or whole plant tissue, pollen-mediated transformations,
25 infection by a recombinant virus or phage agent, such as the modified ToLCV or an Agrobacterium-mediated transformation, and the like. Exemplary vectors for conducting some of the above methods include pBIN19 (Bevan et al, Nucl. Acids Res., 12:8711, 1984; GenBank Accession number U09365), pMON316 or pMON
30 available from Monsanto (St. Louis, MO), pGA482 (An et al, Plant Physiol., 81:86, 1986), pCGN1547 (McBride et al, Plant Mol. Biol., 14:269, 1990), pPZP100 (Ajdukiewicz et al, Plant Mol.

Biol., 25:989, 1994, and GenBank Accession number U10456), pMOG410, and the like.

C. Transgenic Plants

5 The invention further contemplates a transgenic plant containing a nucleotide sequence of this invention for expressing the ssDNA-binding protein. The transgenic plant contains an expression cassette as defined herein as a part of the plant, the cassette having been introduced by transformation
10 of a plant with a vector of this invention.

Methods for producing a transgenic plant useful in the present invention are described in United States Patent Nos. 5,188,642; 5,202,422; 5,234,834; 5,463,175; and 5,639,947, the disclosures of which are hereby incorporated by reference.

15 Techniques for transforming a wide variety of plant species are also well known and described in the technical and scientific literature. See, for example, Weising et al, Ann. Rev. Genet., 22:421-477, 1988. A constitutive or inducible promoter is operably linked to the desired heterologous DNA
20 sequence encoding a ssDNA-binding protein of this invention in a suitable vector. The vector comprising a promoter fused to the heterologous DNA will typically contain a marker gene which confers a selectable phenotype on plant cells. For example, the
25 resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorsulfuron or Basta. Such selective marker genes are useful in protocols for the production of transgenic plants.

DNA constructs containing the expression cassette can be
30 introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the DNA of the plant

cell using techniques such as electroporation and microinjection of plant cell protoplasts. Alternatively, the DNA constructs can be introduced directly to plant tissue using biolistic methods, such as DNA micro-particle bombardment. In addition, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al, EMBO J., 3:2717-2722, 1984. Electroporation techniques are described in Fromm et al, Proc. Natl. Acad. Sci. USA, 82:5824, 1985. Biolistic transformation techniques are described in Klein et al, Nature 327:70-73, 1987. The full disclosures of all references cited are incorporated herein by reference.

A variation involves high velocity biolistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al, Nature, 327:70-73, 1987). Although typically only a single introduction of a new nucleic acid segment is required, this method particularly provides for multiple introductions.

Agrobacterium tumefaciens-mediated transformation techniques are well described in the scientific literature. See, for example Horsch et al, Science, 233:496-498, 1984, and Fraley et al, Proc. Natl. Acad. Sci. USA, 90:4803, 1983. More specifically, a plant cell, an explant, a meristem or a seed is infected with *Agrobacterium tumefaciens* transformed with the segment. Under appropriate conditions known in the art, the

transformed plant cells are grown to form shoots, roots, and develop further into plants. The nucleic acid segments can be introduced into appropriate plant cells, for example, by means of the Ti plasmid of *Agrobacterium tumefaciens*. The Ti plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and is stably integrated into the plant genome (Horsch et al, Science, 233:496-498, 1984; Fraley et al, Proc. Nat'l. Acad. Sci. U.S.A., 80:4803, 1983).

Ti plasmids contain two regions essential for the production of transformed cells. One of these, named transfer DNA (T DNA), induces tumor formation. The other, termed virulent region, is essential for the introduction of the T DNA into plants. The transfer DNA region, which transfers to the plant genome, can be increased in size by the insertion of the foreign nucleic acid sequence without its transferring ability being affected. By removing the tumor-causing genes so that they no longer interfere, the modified Ti plasmid can then be used as a vector for the transfer of the gene constructs of the invention into an appropriate plant cell, such being a "disabled Ti vector".

All plant cells which can be transformed by *Agrobacterium* and whole plants regenerated from the transformed cells can also be transformed according to the invention so as to produce transformed whole plants which contain the transferred foreign nucleic acid sequence.

There are various ways to transform plant cells with *Agrobacterium*, including:

(1) co-cultivation of *Agrobacterium* with cultured isolated protoplasts,

(2) co-cultivation of cells or tissues with *Agrobacterium*,
or

(3) transformation of seeds, apices or meristems with Agrobacterium.

Method (1) requires an established culture system that allows culturing protoplasts and plant regeneration from
5 cultured protoplasts.

Method (2) requires (a) that the plant cells or tissues can be transformed by Agrobacterium and (b) that the transformed cells or tissues can be induced to regenerate into whole plants.

Method (3) requires micropropagation.

10 In the binary system, to have infection, two plasmids are needed: a T-DNA containing plasmid and a vir plasmid. Any one of a number of T-DNA containing plasmids can be used, the only requirement is that one be able to select independently for each of the two plasmids.

15 After transformation of the plant cell or plant, those plant cells or plants transformed by the Ti plasmid so that the desired DNA segment is integrated can be selected by an appropriate phenotypic marker. These phenotypic markers include, but are not limited to, antibiotic resistance,
20 herbicide resistance or visual observation. Other phenotypic markers are known in the art and may be used in this invention.

The present invention embraces use of the expression vectors described herein in transformation of any plant, including both dicots and monocots. Transformation of dicots is
25 described in references above. Transformation of monocots is known using various techniques including electroporation (e.g., Shimamoto et al, Nature, 338:274-276, 1992; ballistics (e.g., European Patent Application 270,356); and Agrobacterium (e.g., Bytebier et al, Proc. Nat'l Acad. Sci. USA, 84:5345-5349, 1987).

30 Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the desired transformed phenotype.

Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium typically relying on a biocide and/or herbicide marker which has been introduced together with the nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al, Handbook of Plant Cell Culture, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, Regeneration of Plants, Plant Protoplasts, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally by Klee et al, Ann. Rev. Plant Phys., 38:467-486, 1987.

One of skill will recognize that, after an expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

D. Compositions

Also contemplated is a composition useful for introducing a nucleotide sequence of this invention into plants. The composition is useful for producing resistance to a ssDNA virus that infects plants, and comprises an effective amount of the nucleotide sequence according to the invention for introducing the ssDNA-binding protein into a plant, and depends upon the method used for introducing the protein to the plant. For example, using direct DNA uptake by protoplast, the composition is a aqueous solution containing nucleic acid and buffers to facilitate uptake by protoplast, as is well known. For transformation by an Agrobacterium vector, the composition contains a suspension of Agrobacteria containing the nucleotide

sequence capable of expressing the ssDNA-binding protein.

E. Systems for Use

The present invention also contemplates a system,
5 preferably in kit form, useful for practicing the methods of the
present invention. Thus, the kits are useful for introducing a
nucleic acid sequence of the present invention into a plant as
practiced in the methods of this invention.

The kit comprises, in an amount sufficient to perform at
10 least one introduction, a composition of the present invention
comprising a nucleic acid molecules which comprise a nucleotide
sequence capable of expressing a ssDNA-binding protein according
to the present invention, present in a packaging material or
container for providing the system.

15 Instructions for use of the packaged reagent are also
typically included in the system in the form of a label or
packaging insert.

"Instructions for use" typically include a tangible
expression describing the contents of the reagent(s) in the
20 system or at least one method parameter such as the relative
amounts of composition and plant to be admixed, procedures for
contacting the plant, temperature, buffer conditions and the
like for practicing a method of the invention. Typically, the
instructions will recite the method for contacting a plant to
25 introduce the ssDNA-binding protein of the invention into a
plant, and thereby inhibit symptoms of ssDNA virus infection in
the plant.

The reagent species, infectious agent, virus or phage,
nucleic acid molecule or expression vector for practicing a
30 method described herein can be provided in solution, as a liquid
dispersion or as a substantially dry power, e.g., in lyophilized
form.

The term "package" refers to a solid matrix or material such as glass, plastic (e.g., polyethylene, polypropylene and polycarbonate), paper, foil and the like capable of holding within fixed limits a reagent such as a polynucleotide, transformation agent, infectious virus or phage of the present invention. Thus, for example, a package can be a bottle, vial, plastic and plastic-foil laminated envelope or the like container used to contain a contemplated composition.

The package can contain one or more unit dosages of the composition of the invention, or may alternatively be packaged with the composition provided in bulk.

A system of this invention may comprise a carrier means being compartmentalized to receive in close confinement one or more container means such as vials, tubes, and the like, each of the container means comprising one of the separate elements to be used in the method. For example, one of the container means may comprise a composition for infecting a plant. The kit may also have containers containing any other reagents used to practice the methods of the invention.

Other uses will be apparent to one skilled in the art in light of the present disclosures and the examples that follow.

EXAMPLES

The following examples are provided by way of illustration and not limitation.

1. Plasmid constructs

Infectious clones of the A and B components of tomato leaf curl virus (Padidam et al, J. Gen. Virol., 76:25-35, 1995) were employed to generate the virus constructs used herein. The genome organization of ToLCV and schematic representation of virus constructs used are shown in Figure 1 and the detailed

descriptions and methods of construction of each of the plasmid are summarized in Table 1. Partial head to tail dimers made from these constructs were used to infect *Nicotiana benthamiana* plants and *N. tabacum* BY2 protoplasts.

5

TABLE 1

Description and method of construction of viral DNAs

Construct	Description and method of construction
10 AV2-CP ⁻	A double mutant of AV2 and coat protein (CP) in which Met1 codon of AV2 was changed to termination codon and Arg66 codon of CP was frame shifted. The mutant has been described earlier as M1te/R66fr (Padidam et al, <u>Virology</u> , 224:390-404, 15 1996).
g5AV2-CP ⁻	A 264-bp sequence coding for gene 5 (g5) protein from bacteriophage M13mp18 vector was amplified by PCR (10 cycles) and cloned between Afl III (nt 20 125) and Sty I (nt 479) sites resulting in replacement of AV2 ORF and overlapping 5' CP ORF sequences with g5.
25 g5- ⁻ AV2-CP ⁻	A negative control of g5AV2-CP ⁻ construct in which Met1 codon of g5 was mutated to a termination codon.
30 CP ⁻	A mutant of CP made by end-filling and religation at the unique Sty I site (nt 479) causing frame shift at Arg66 codon and termination after amino acid (aa) 69. The mutant has been described earlier as R66fr (Padidam et al, <u>Virology</u> ,

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protoplasts using the anti-Flag antibody.

CP66:GUS

A 1806-bp DNA fragment coding for β -glucuronidase (GUS) protein (Jefferson et al, Plant Mol. Biol. Rep., 5:387-405, 1987) was PCR amplified (10 cycles) and cloned between Sty I (nt 479) and Hind III (nt 1041) sites of A component. The Hind III site was created at the codon for Tyr251 of CP [15-bp before the termination codon, (Padidam et al, Virology, 224:390-404, 1996)]. This facilitated replacement CP sequence with other sequences.

GUSAV2-CP-

A 1869-bp Nco I to EcoR I DNA fragment coding for GUS protein was cloned between Afl III (nt 125) and Hind III (nt 1041) sites of A component after blunt ending the EcoR I site on the GUS gene and Hind III site on A component DNA.

GFPVAV2-CP-

A 717-bp with Nco I to BamH I DNA fragment coding for green fluorescent protein [GFP - S65C, M153T, V163A; (Reichel et al, Proc. Natl. Acad. Sci. USA, 93:5888-5893, 1996)] was cloned between Afl III (nt 125) and Sph I (nt 836) sites of A component after blunt ending the BamH I site on the GFP gene and Sph I site on A component DNA.

BV1AV2-CP-

A 849-bp sequence coding for BV1 from B component of ToLCV was amplified by PCR (10 cycles) and cloned between Afl III (nt 125) and Hind III (nt 1041) sites of A component.

FBV1AV2-CP⁻ Similar to BV1AV2-CP⁻ except that sequence coding for 9 aa Flag peptide was added before the Met1 codon of BV1. Flag epitope was added to immunolocalize the BV1 protein in protoplasts using the anti-Flag antibody.

BC1AV2-CP⁻ A 882-bp sequence coding for BC1 from B component of ToLCV was amplified by PCR (10 cycles) and cloned between Afl III (nt 125) and Hind III (nt 1041) sites of A component.

TBC1AV2-CP⁻ Similar to BC1AV2-CP⁻ except that sequence coding for 11 aa T7 [MASMTGGQQMG; (Krek et al, Cell, 78:161-172, 1994)] epitope was added before the Met1 codon of BC1. T7 tag epitope was added to immunolocalize the BC1 protein in protoplasts using the anti-T7 tag antibody.

CP66:6G:BC1 A 900-bp sequence coding for 6 glycines and BC1 from B component of ToLCV was amplified by PCR (10 cycles) and cloned between Sty I (nt 479) and Hind III (nt 1041) sites.

BC1⁻ B component DNA in which a frame-shift mutation of BC1 was created by deleting the 3' overhang and religating at the Pst I site (nt 2075). Described earlier as BC1M (Padidam et al, Virology, 224:390-404, 1996).

2. Protoplast and plant inoculations

N. benthamiana plants (two week-old seedlings grown in Magenta boxes) and protoplasts isolated from BY2 suspension

cells were infected with viral DNAs as described earlier (Padidam et al, J. Gen. Virol., 76:25-35, 1995; Padidam et al, Virology, 224:390-404, 1996). Protoplasts were collected from cultures 48 h postinoculation for DNA isolation,

5 immunoprecipitation reactions, and western blot analysis. Plants were scored for symptoms, and the newly formed upper leaves were collected for Southern blot analysis 22 to 25 days following inoculation. To study the local and systemic movement of the virus expressing green fluorescent protein [GFP; (Chalfie et al, 10 Science, 263:802-805, 1994)], bottom leaves of four-week old seedlings (10 plants per construct) were inoculated. Inoculated and upper non-inoculated leaves were observed at three day intervals for fifteen days under a fluorescence microscope for the detection of fluorescence emitted by GFP. In all experiments 15 that involved plants, wild type B component DNA, which is essential for systemic spread and symptom development, was included.

3. Southern blotting

20 Total DNA was isolated from protoplasts (Mettler et al, Plant Mol. Biol. Rep., 5:346-349, 1987) and plants (Dellaporta et al, Plant Mol. Biol. Rep., 1:19-21, 1983) and electrophoresed in 1% agarose gels (without ethidium bromide) and transferred to Hybond nylon membranes (Amersham, Arlington Heights, IL) using 25 the standard protocols (Sambrook et al, Molecular Cloning: A laboratory manual., Cold Spring harbor laboratory press. Cold Spring harbor, N.Y., 1989). Hybridization reactions were performed using a randomly primed ³²P-labeled A component specific probe (the 900 bp Afl II-Pst I fragment containing ORFs 30 AC1, AC2, and AC3). The amount of viral ss and dsDNA (super coiled, linear, open circular, and dimeric forms) was quantitated by exposing the Southern blots to storage phosphor

screen plates and counting on a PhosphorImager (Molecular Dynamics, Sunnyvale, CA). The ssDNA form was confirmed by its susceptibility to S1 and mungbean nucleases (Padidam et al, Virology, 224:390-404, 1996). In the absence of ethidium

5 bromide, the super coiled viral DNA form runs ahead of the ssDNA form.

4. Immunoprecipitation and western blotting

For immunoprecipitation reactions, protoplasts infected
10 with the virus A component expressing CP66:6G:g5 protein tagged with Flag epitope (FCP66:6G:g5, Table 1) were lysed with a hand held polytron in NP40 buffer [50 mM Tris-HCl (pH 7.5), 1% NP40, with 0.15, 0.25, 0.50, 0.75, or 1.0 M NaCl] or RIPA buffer [50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1% NP40, 0.5% DOC, 0.1% SDS]
15 containing a cocktail of protease inhibitors (Boehringer Mannheim, Indianapolis, IN). Cell debris was removed by centrifugation at 4°C for 10 min at 15,000 x g. Lysates were immunoprecipitated with anti-Flag monoclonal M2 antibody covalently linked to agarose (Sigma, St. Louis, MO). Immune
20 complexes were washed four times with NP40 or RIPA buffer and once with Tris-buffered saline [50 mM Tris-HCl (pH 7.5), 150 mM NaCl]. Half of each sample was heated in Laemmli sample buffer, fractionated by SDS-PAGE (13% acrylamide), and transferred to PVDF membrane (Schleicher & Schuell, Keene, NH).
25 Immunoprecipitated protein was visualized with anti-Flag M2 antibody using ECL-western blot reagents (Pierce, Rockford, IL). The remaining half of the immune complex collected by this procedure was used for isolating the viral DNA. Whole cell protein extracts for direct western blotting were prepared by
30 boiling the protoplast pellets with equal volume of 2 x Laemmli sample buffer.

5. Immunofluorescence

Protoplasts transfected with viral constructs were cultured on chamber slides (Nalge Nunc, Rochester, NY) for 48h, fixed with 3% paraformaldehyde in PBSEM [50 mM phosphate (pH 6.95), 150 mM NaCl, 5 mM EGTA, 5 mM MgSO₄] for 30 min, and permeabilized with 100% methanol at -20°C for 10 min. The cells were washed two times with PBSEM containing 0.5% Tween 20 for 30 min. CP66:6G:g5 protein tagged with Stag epitope (CP66:Stag:6G:g5, Table 1) was detected with the S-protein coupled to FITC (Novagen, Madison, WI). The fifteen amino acid long Stag peptide was inserted after Arg66 of the CP to construct the CP66:Stag:6G:g5 protein. Flag epitope-tagged BV1, T7 epitope-tagged BC1, CP and β -glucuronidase (GUS) (Table 1) were detected with anti-Flag M2 antibody (Sigma, St. Louis, MO), anti-T7 tag antibody (Novagen, Madison, WI), anti-CP antisera (Padidam et al, Virology, 224:390-404, 1996), and anti-GUS antisera (5'-3', Boulder, CO) diluted 1:100 in PBS, respectively. After incubation in primary antibody for 1 h at 30°C, the cells were washed as before and incubated with FITC or rhodamine conjugated IgGs (Pierce, Rockford, IL) at a dilution of 1:100. The cells were mounted in Fluoromount G (Electron Microscopy Sciences, Fort Washington, PA) and viewed with a Nikon fluorescence microscope or Olympus confocal microscope (for detecting T7 epitope-tagged BC1 protein).

6. ToLCV expressing gene 5 protein or CP66:6G:g5 protein accumulates ssDNA to wild type levels in protoplasts

Previous reports work with ToLCV have shown that viral CP and AV2 are not required for virus replication in protoplasts whereas AV2 is required for efficient movement in plants (Padidam et al, Virology, 224:390-404, 1996). Coat protein is not essential for systemic movement and symptom development in

ToLCV. However, mutations in the CP sequence caused a marked decrease in ssDNA accumulation in *N. benthamiana* and tomato plants and in BY2 protoplasts while increasing dsDNA accumulation in protoplasts. Virus that contained mutations in the AV2 plus CP behaved like AV2 mutants in plants (i.e., poor virus movement and very mild symptoms) and like CP mutants in protoplasts (i.e., decrease in ssDNA and increase in dsDNA accumulation).

The present plasmid constructs provide information on the effects of gene 5 protein (g5p) from *E. coli* phage M13 (Salstrom et al, J. Mol. Biol., 61:489-501, 1971) on replication of ToLCV. Each of these mutations are described in Table 1 and Figure 1. The AV2 and the overlapping 5' portion of the CP ORF were replaced with the g5p and assayed its effect on virus replication in protoplasts. In these experiments protoplasts were inoculated with wild type (wt) or other mutants, as described below. The modified A component, designated g5AV2-CP⁻, led to accumulation of ssDNA to the same levels as did infections with wt virus A component (Table 2; Figure 2, lanes 1 and 3). However, dsDNA accumulation was high (3 to 6 fold higher than wt levels) and similar to accumulation in virus with mutations in CP (Table 2; Figure 2, lanes 2-4). Infection by virus in which the g5 gene was mutated to prevent its translation (g5-⁻AV2-CP⁻, Table 1) behaved like virus infections with A component mutants AV2-CP⁻ and CP⁻ (Table 2; Figure 2, lane 4). Since AV2 is required for efficient virus movement in plants another construct was made in which g5 was fused to CP at Arg66 without affecting the AV2 ORF (CP66:g5, Table 1). CP66:g5 virus A component also led to accumulation of ssDNA, but to lower levels than g5AV2-CP⁻ DNA (Table 2; Figure 2, lane 6). To evaluate whether the N-terminal 66 amino acids (aa) of CP interfered with the ability of g5p to bind DNA, a linker of six

glycine residues was introduced between Arg66 of CP and g5 to separate the CP domain from the g5p (CP66:6G:g5). Addition of the linker restored the ability of the CP66:6G:g5 virus A component to accumulate ssDNA to levels comparable to those of g5AV2-CP⁻ (Table 2; Figure 2, lane 7). A control construct in which the g5 portion of the fusion protein was not translated (CP66:g5⁻) failed to accumulate ssDNA (Table 2; Figure 2, lane 8). The ability of virus A component expressing CP66:6G:g5 protein to accumulate ssDNA was not due to N-terminal 66 aa of the CP was suggested by the facts that the virus A component expressing g5p alone accumulated ssDNA and the virus A components expressing CP66:6G:BC1 (see below) or CP66:6G:AV2 failed to accumulate ssDNA.

TABLE 2

Effect of gene 5 protein on replication and movement of tomato leaf curl virus in *Nicotiana tabacum* protoplasts and *N. benthamiana* plants

Protoplast inoculations

<u>Virus</u>	<u>ssDNA^a</u>	<u>dsDNA^a</u>
Wild type ^c	100	100
AV2-CP ⁻	<1 (0-0.03)	506 (427-584)
g5AV2-CP ⁻	102 (79-133)	409 (349-573)
g5-CP ⁻	7 (5-12)	384 (210-779)
CP ⁻	5 (2-7)	241 (148-369)
CP66:g5	17 (8-27)	442 (345-576)
CP66:6G:g5	118 (34-234)	517 (133-784)
CP66:g5 ⁻	9 (3-14)	424 (179-789)

Plant inoculations

<u>Virus</u>	<u># of plants inoculated</u>	<u>Symptom type</u>	<u>ssDNA^b</u>	<u>dsDNA^b</u>
Wild type ^c	20	Severe	100	100
AV2-CP ⁻	10	Very mild ^d	0.3 (0.05-0.5)	11 (9.6-17)

	g5AV2-CP ⁻	20	Very mild ^d	0.6 (0.1-2.7)	15.2 (6.2-49.2)
5	g5- ⁻ AV2-CP ⁻	20	Very mild ^d	0.1 (0.0-0.2)	5.7 (0.0-11.4)
	CP ⁻	20	Severe ^e	4.3 (2.6-6.5)	102 (65-139)
10	CP66:g5	20	mild	2.2 (0.8-4.2)	30.6 (15.3-55.1)
15	CP66:6G:g5	30	Very mild ^d	0.9 (0.4-1.7)	10.9 (5.5-14.7)
20	CP66:g5 ⁻	20	Severe ^e	4.0 (1.8-6.1)	139.7 (56.0-197.7)

^a The values represent the average amount (range) of single-stranded (ss) and double-stranded (ds) A component DNA in five independent protoplast transfections per mutant. Protoplasts (~10⁶) were transfected with 2 µg of A component DNA and 40 µg of herring sperm DNA. Viral DNA was quantitated on Southern blots using the "PhosphorImager" from Molecular Dynamics.

^b The values are average (range) amounts of viral DNA in twelve inoculated plants per virus construct except for AV2-CP⁻ for which the values are averages of four plants. Each plant was inoculated with 0.5 µg of A and 0.5 µg of wild type B component DNA, which is essential for viral movement and symptom development.

^c The amount of viral DNA in protoplasts and plants inoculated with the wild type viral DNA were assigned a value of 100.

^d Many plants did not show symptoms.

^e Severe symptoms like in plants inoculated with the wild type virus but without intense chlorosis.

Geminiviruses replicate in the nucleus (Accotto et al, Virology, 195:257-259, 1993; Nagar et al, Plant Cell, 7:705-719, 1995), so it is likely that in order to cause the accumulation of ssDNA the CP66:6G:g5 and g5 proteins must be present in the nucleus. To immunolocalize the CP66:6G:g5 fusion protein in protoplasts, the Stag epitope was inserted between

Arg66 of the CP and the glycine linker (CP66:Stag:6G:g5, Table 1). At 48 h after infection protoplasts were fixed and subjected to reactions with S-protein coupled to FITC. The CP66:Stag:6G:g5 protein as well as the wt CP (detected with anti-CP antisera) were localized to the nucleus (Figure 3A and 3B). When GUS protein was produced as a fusion protein with the N-terminal 66 aa of CP (CP66:GUS), the GUS (detected with anti-GUS antisera) was also localized to the nucleus (Figure 3C). This indicated that the N-terminal 66 aa of the CP contained a nuclear localization signal.

g5p contains a nuclear localization signal as shown by fusing g5 sequence to the sequence coding for GUS at the N-terminus. The g5:GUS fusion protein (expressed in g5:GUSAV2-CP⁻ virus A component, Table 1) and unfused GUS protein (expressed in GUSAV2-CP⁻ virus A component, Table 1) remained in the cytoplasm (Figure 3D and 3E), indicating that g5p has no nuclear localization signal. The g5p most likely entered the nucleus in a passive manner based on its size (9.7 kDa) which is smaller than the permeability barrier of the nuclear envelop (Dingwall et al, Ann. Rev. Cell Biol., 2:367-390, 1986).

7. Movement of ToLCV expressing CP66:6G:g5 protein is impaired in plants

N. benthamiana plants were inoculated with selected virus constructs to determine the effect of g5p on virus spread: in these studies B component DNA was coinoculated with A component onto *N. benthamiana* seedlings. As expected, plants inoculated with A component mutants AV2-CP⁻, g5AV2-CP⁻, or g5-AV2-CP⁻ plus B component showed very mild or no symptoms and all inoculated plants accumulated low levels of viral DNA (Table 2). A previously reported ToCLV mutant (Padidam et al, Virology, 224:390-404, 1996) that did not produce CP but

produced AV2 (CP⁻) developed severe disease symptoms and wt levels of dsDNA on systemic infections (Table 2). Surprisingly, plants inoculated with the virus expressing CP66:6G:g5 protein showed very mild or no symptoms even though the virus contained
5 an intact AV2 gene (Table 2). These plants accumulated low levels of viral DNA similar to plants inoculated with AV2-CP⁻ virus (Table 2). Plants inoculated with the virus expressing CP66:g5 protein (which accumulated ssDNA to a lower level than CP66:6G:g5 virus in protoplasts) showed mild symptoms and
10 accumulated moderate levels of dsDNA. The impaired movement of the virus expressing g5p was due to possible toxic effects of g5p. No differences in protoplast viability or in appearance of plant leaves inoculated with wt virus or virus expressing g5p were detected that might suggest toxicity of g5p.

15 The cell to cell and long distance movement of ToLCV expressing CP66:6G:g5 protein was examined by utilizing green fluorescent protein (GFP) as a visible marker for virus movement. Plants were inoculated with A component DNA expressing GFP in place of AV2 and CP (GFP-CP⁻) alone, or coinoculated
20 with A component DNA of the wt, CP66:6G:g5, or CP66:g5⁻ construct. GFP-CP⁻ virus was expected to move inefficiently in plants as it does not encode AV2; it was expected to move efficiently when complemented by another virus encoding AV2. GFP could not be detected in plants by 3 d post inoculation, but it
25 was present on inoculated and upper leaves by day 6 in the majority of the plants inoculated with GFP-CP⁻ plus wt A component, or GFP-CP⁻ plus CP66:g5⁻ viruses (Figure 3H, 3I; only data on plants inoculated with GFP-CP⁻ plus CP66:g5⁻ viruses is shown). The virus expressing GFP continued to spread
30 to upper and newly emerging leaves in these plants (Figure 3J, 3K). GFP was observed in veins, mesophyll and epidermal cells, and was present in large areas of the leaf in plants inoculated

with GFP-CP- plus CP66:g5- viruses. In contrast, GFP was restricted to small spots on the inoculated leaves of most of the plants inoculated with GFP-CP-, or GFP-CP- plus CP66:g5 viruses (Figure 3L, 3M; only data on plants inoculated with GFP-CP- plus CP66:g5 viruses is shown). These plants also showed GFP staining in some adjacent and newly emerging leaves, but mostly restricted to veins (Figure 3N, 3O, 3P). These results indicated that expressing the g5p in place of CP has decreased the efficiency of the virus systemic movement.

8. In vivo binding of CP66:g5 protein to viral DNA

The accumulation of viral ssDNA in protoplasts inoculated with virus A component expressing g5p or CP66:g5 protein indicated that g5p binds to ssDNA. In verification, protoplasts were inoculated with virus A component expressing Flag epitope-tagged CP66:g5 protein (FCP66:g5, Table 1) and immunoprecipitated the Flag epitope-tagged CP66:g5 protein using anti-Flag antibody and characterized the viral DNA that coimmunoprecipitated with the CP66:g5 protein by Southern blotting. The immunoprecipitations were performed under different salt (1% NP40 buffer with 0.15 to 1.0 M NaCl) conditions and in the presence of 0.1% SDS, 0.5% DOC and 1% NP40 detergents (RIPA buffer) to assay the affinity of binding. Flag epitope-tagged CP66:g5 protein was immunoprecipitated in all the buffer conditions tested; the amount of protein immunoprecipitated increased with the increase in salt concentration. (Figure 4A). The amount of coimmunoprecipitated ssDNA increased up to 0.5 M salt and decreased at higher concentrations (Figure 4B), indicating the g5p-ssDNA complex was destabilized in buffer that contained 1 M salt. Immunoprecipitation in RIPA buffer also resulted in reduced amount of precipitated DNA (Figure 4B). These results showed

that g5p bound to viral ssDNA and 1M salt (in NP40 buffer) dissociated g5p from viral DNA.

9. Role of BV1 and BC1 movement proteins in spread of ToLCV

5 Together, the above results indicate that CP66:6G:g5 protein is localized to the nucleus and binds stably to ToLCV virus DNA in vivo, and ToLCV expressing CP66:6G:g5 does not move efficiently in plants. The inefficient movement of ToLCV expressing CP66:6G:g5 protein may be due to interference of g5p
10 with the function of BV1 or BC1 movement proteins of ToLCV. In squash leaf curl virus (SLCV), BV1 (referred to as BR1 in SLCV) protein, but not BC1 (referred to as BL1 in SLCV), binds to ssDNA in vitro (Pascal et al, Plant Cell, 6:995-1006, 1994). BV1 and BC1 of SLCV interact with each other in a cooperative
15 manner; in protoplasts BV1 localizes to the nucleus in the absence of BC1 but localizes to the cell periphery in the presence of BC1 (Sanderfoot et al, Plant Physiol., 110:23-33, 1996; Sanderfoot et al, Plant Cell, 7:1185-1194, 1995). Both BV1 and BC1 are required for the systemic spread and symptom
20 development of ToLCV (Padidam et al, Virology, 224:390-404, 1996). To determine if BV1 and BC1 of ToLCV have similar functions as BV1 and BC1 of SLCV, BV1 and BC1 of ToLCV were immunolocalized and examined for their ability to complement viral ssDNA accumulation of CP mutants. For these experiments
25 BV1 and BC1 genes were fused to sequences coding for Flag epitope tag and T7 epitope tag, respectively, and inserted in place of AV2 and CP in the A component (FBV1AV2-CP⁻ and TBC1AV2-CP⁻, Table 1). In protoplasts inoculated with FBV1AV2-CP⁻ construct, BV1 protein accumulated in the nucleus (detected
30 using anti-Flag antibody, Figure 3F) while in protoplasts inoculated with TBC1AV2-CP⁻, the BC1 protein was localized to the cell periphery (detected using anti-T7 tag antibody, Figure 3G).

Expression of BV1 protein in place of AV2 and CP protein (BV1AV2-CP-) also led to the accumulation of ssDNA of the A component (Table 3; Figure 2, lane 9). The binding affinity of BV1 protein tagged with Flag epitope to viral DNA in protoplasts inoculated with FBV1AV2-CP- DNA was determined by immunoprecipitation reactions similar to those described in Figure 4. The binding affinity of BV1 protein to viral ssDNA was similar to the binding affinity of CP66:6G:g5 protein to viral DNA. In contrast to results obtained with the A component DNA expressing BV1, A component DNA expressing BC1 protein in place of AV2 and CP (BC1AV2-CP-) did not accumulate ssDNA (Table 3; Figure 2, lane 10). Since BC1 protein was localized to the cell periphery, BC1 was fused to N-terminal 66 aa of the CP (CP66:6G:BC1) to direct it to the nucleus. Virus A component DNA expressing the CP66:6G:BC1 protein also did not accumulate ssDNA (Table 3; Figure 2, lane 11) showing that BC1 movement protein may not bind to viral ssDNA or the binding affinity was not sufficiently strong enough to result in the accumulation of ssDNA. These results show that BV1 is localized to the nucleus in the absence of BC1, and BV1 binds to viral ssDNA in vivo.

TABLE 3

Complementation by BV1 and BC1 movement proteins for the accumulation of tomato leaf curl virus ssDNA in protoplasts^a

5

	<u>A component</u>	<u>B component</u>	<u>ssDNA</u>	<u>dsDNA</u>
	Wild type	none	100	100
	BV1AV2-CP ⁻	none	86 (50-121)	230 (119-195)
	FB1AV2-CP ⁻	none	33 (25-54)	47 (40-58)
10	BC1AV2-CP ⁻	none	2 (1-3)	224 (162-288)
	CP66:6G:BC1	none	5 (1-10)	214 (180-267)
	Wild type	Wild type	57 (37-78)	61 (42-81)
	Wild type	BC1 ⁻	48 (38-58)	50 (40-60)
	AV2-CP ⁻	Wild type	2.4 (1.2-3.6)	131 (76-187)
15	AV2-CP ⁻	BC1 ⁻	2.7 (1.5-4.0)	135 (82-188)
	CP ⁻	Wild type	2.5 (1.6-3.3)	100 (78-121)
	CP ⁻	BC1 ⁻	2.9 (2.1-3.7)	106 (98-113)

^a Protoplasts were transfected with 2 μ g of A component DNA with or without 10 μ g of B component DNA. Viral single-stranded (ss) and double-stranded (ds) DNA was quantitated on Southern blots using "PhosphorImager" and the values represent the average amount (range) of viral DNA in two to five independent transfections.

25

In plants inoculated with ToLCV A component containing CP66:6G:g5 gene plus wt B component the expression of CP66:6G:g5 protein is controlled by the relatively strong CP promoter. The CP66:6G:g5 protein produced from the A component may out-compete with the BV1 protein (expressed from the B component) for DNA binding if the amount of BV1 made under its own promoter is relatively low. We conducted an experiment to determine if BV1, expressed under its own promoter on the B component, can lead to accumulation of ssDNA. Note that BV1 led to accumulation of ssDNA when expressed in place of CP on A component (Table 3). However, very little viral ssDNA accumulated in protoplasts coinoculated with A component DNA with mutations in CP (CP⁻) plus wt B component DNA (i.e., expressing both BV1 and BC1) or B component with a mutation in BC1 (BC1⁻; i.e., expressing only BV1) (Table 3; Figure 2, lanes 12-15). The failure of BV1 to cause

40

accumulation of ssDNA when expressed from the B component appeared to be due to low levels of BV1 protein being made; no BV1 protein was detected in protoplasts coinoculated with A component DNA and B component DNA expressing Flag epitope-tagged BV1 by immunolocalization and western blotting procedures. These results show that the B component promoter driving the expression of BV1 is not as strong as when the gene was expressed from the CP promoter on the A component.

10. Discussion of Examples 1-9

A non-specific ssDNA binding protein (g5) was expressed in place of CP and was monitored for the accumulation of ssDNA to determine if it could serve as a substitute for CP in Geminivirus. The g5p from E. coli phage M13 was chosen because of its small size (9.7 kDa) and lack of any enzymatic function in DNA replication. The role of g5p in replication of M13 and other filamentous phages has been extensively studied (Rasched et al, Microbiol. Rev., 50:401-427, 1986) and its structure has been determined (Skinner et al, Proc. Natl. Acad. Sci. USA, 91:2071-2075, 1994). Gene 5 protein binds newly formed viral ssDNA tightly, cooperatively, and in a sequence independent manner, and protects it from degradation by E. coli nucleases.

It is shown that g5p can bind to ToLCV ssDNA in plant cells and ToLCV expressing g5p or g5p fused to N-terminal 66 aa of the CP accumulated ssDNA to wt levels. The binding of g5p to viral ssDNA in vivo was similar to the binding of g5p to M13 ssDNA in vitro (Anderson et al, Biochemistry, 14:907-917, 1975). Though g5p compensated for the lack of CP by causing an increase in accumulation of ssDNA of ToLCV, it did not reduce the amount of dsDNA to wt levels. BV1 movement protein (when expressed in place of CP) also behaved like g5p in that it did not down-regulate the dsDNA to wt levels. If CP regulates the levels of

ss and dsDNA by depleting the ssDNA available for conversion to dsDNA, expression of g5p or BV1 could be expected to result in normal amounts of dsDNA. The fact that it did not suggests that CP may have a direct role in regulating virus replication,

5 possibly by inhibiting minus-strand synthesis or by regulating gene expression. The CP of alfalfa mosaic virus (AlMV), a virus with a ssRNA(+) genome, has been shown to play a direct role in regulation of plus- and minus-strand RNA synthesis. The AlMV CP was found in tight association with the viral RNA polymerase and
10 inhibited minus-strand synthesis while stimulating plus-strand synthesis. Recent results on SLCV suggests that CP acts to signal the switch from viral dsDNA replication to ssDNA replication, or to sequester virion ssDNA from replication pool without fully encapsidating it. Purification of geminivirus
15 replication complexes is needed to directly assess the role of CP in replication.

Plants infected with virus that encodes CP66:6G:g5 protein show very mild symptoms and accumulate low levels of viral DNA when infected protoplasts accumulated high levels of viral DNA.
20 This occurs because by binding to viral ssDNA, g5p affects virus movement by interfering with the function of BV1 movement protein. BV1 of ToLCV was localized to the nucleus in infected protoplasts and bound to viral ssDNA in vivo; whereas BC1 was localized to the cell periphery and did not complement viral
25 ssDNA accumulation even when it was directed to the nucleus as a fusion to the nuclear localizing signal of CP. Recent studies on the role of BV1 and BC1 in SLCV movement have shown that BV1 localizes to the nucleus, binds to ssDNA in vitro, and functions as a nuclear shuttle protein. BC1 of SLCV is localized to the
30 cell periphery in protoplasts and is associated with endoplasmic reticulum-derived tubules in developing phloem cells of systemically infected pumpkin seedlings. Based on these

results, a model for SLCV was proposed in which BC1 containing tubules serve as a conduit for the transport of BV1, and its associated viral ssDNA, from one cell to another (Ward et al, J. Virol., 71:3726-33, 1997). Studies on TGMV have shown that BV1 interacts with viral ssDNA in vivo and BV1 and BC1 have distinct and essential roles in cell to cell movement as well as systemic movement (Jeffrey et al, Virology., 223:208-218, 1996). ToLCV employs a similar strategy in moving from cell to cell. The poor movement of ToLCV that produces CP66:6g:g5 protein is due to reduced binding of BV1 to viral ssDNA. It should be noted that BV1 did not lead to accumulation of ssDNA of A component that lacked CP when BV1 was expressed under its own promoter from the B component. In plants coinoculated with A component producing CP66:6G:g5 plus A component producing GFP, GFP staining was mostly restricted to small areas, both on inoculated and systemically infected leaves, showing an over all reduction in the efficiency of viral movement than specific interference with cell to cell spread or long distance movement.

The interference with the ToLCV movement due to binding of g5p to viral ssDNA indicates that in this virus ssDNA moves from cell to cell. These results also indicate that expression of g5p in transgenic plants provides a novel way of controlling geminiviruses and that such resistance is effective against all geminiviruses.

In summary, to determine whether the gene 5 protein (g5p), a ssDNA binding protein from Escherichia coli phage M13, could restore the accumulation of ssDNA, ToLCV that lacked the CP gene was modified to express g5p or g5p fused to the N-terminal 66 amino acids of the CP (CP66:6G:g5). The modified viruses led to accumulation of wild type levels of ssDNA and high levels of dsDNA. The accumulation of ssDNA was due to stable binding of g5p to the viral ssDNA. The high levels of dsDNA accumulation

during infections of the modified viruses indicated suggested a direct role for CP in viral DNA replication. ToLCV that produced CP66:6G:g5 protein did not spread efficiently in Nicotiana benthamiana plants and inoculated plants developed only very mild symptoms. In infected protoplasts CP66:6G:g5 protein was immunolocalized to nuclei; this indicates that the fusion protein interferes with the function of BV1 movement protein and thereby prevents spread of the infection.

The foregoing specification, including the specific embodiments and examples, is intended to be illustrative of the present invention and is not to be taken as limiting. Numerous other variations and modifications can be effected without departing from the true spirit and scope of the invention.

What Is Claimed Is:

1. A method for producing in a plant resistance to a single stranded DNA (ssDNA) virus comprising introducing a ssDNA-binding protein of the Inoviridae virus family into said
5 plant.

2. The method of claim 1 wherein said Inoviridae family virus is selected from the group consisting of the Inovirus and Plectrovirus genuses.

3. The method of claim 2 wherein said Inovirus genus
10 virus is selected from the group consisting of Coliphage, enterobacteria phage, Pseudomonas phage, Vibrio phage and Xanthomonas phage species.

4. The method of claim 3 wherein said Coliphage species of virus is selected from the group consisting of AE2, dA, Ec9, f1, fd, HR, M13, ZG/2 and ZJ/2 coliphages.
15

5. The method of claim 1 wherein said ssDNA-binding protein is a coat protein or a gene 5 protein.

6. The method of claim 1 wherein said ssDNA-binding protein is the Coliphage M13 gene 5 protein.
20

7. The method of claim 6 wherein said Coliphage M13 gene 5 protein has the amino acid residue sequence of SEQ ID NO 1.

8. The method of claim 1 wherein said introducing comprises preparing a transgenic plant containing a gene which expresses said ssDNA-binding protein.
25

9. The method of claim 8 wherein said gene comprises a nucleotide sequence shown in SEQ ID NOs 2 or 3.

10. The method of claim 1 wherein said introducing comprises contacting said plant with a composition containing an expression vector capable of expressing said ssDNA-binding
30 protein.

11. The method of claim 10 wherein said expression vector comprises a nucleotide sequence shown in SEQ ID NOs 2 or 3.

12. The method of claim 10 wherein said contacting comprises biolistic gene transfer or direct DNA uptake into protoplast.

13. The method of claim 10 wherein said contacting
5 comprises infection of said plant with a carrier vector

14. The method of claim 13 wherein said carrier vector is an Agrobacterium vector.

15. The method of claim 10 wherein said expression vector is present in a virus particle capable of infecting said plant
10 and expressing said ssDNA-binding coat protein.

16. The method of claim 1 wherein said plant is selected from the group consisting of Abutilon, Acalypha, apple, Ageratum, Althea rosea, Asystasia, Bajra, banana, barley, beans, beet, Blackgram, Bromus, Cassava, chickpea, Chilllies, Chloris,
15 clover, coconut, coffee, cotton, cowpea, Croton, cucumber, Digitaria, Dolichos, eggplant, Eupatorium, Euphorbia, fababean, honeysuckle, horsegum, Jatropha, Leonurus, limabean, Lupin, Macroptilium, Macrotyloma, maize, melon, millet, mungbean, oat, okra, Panicum, papaya, Paspalum, peanut, pea, pepper, pigeon
20 pea, pineapple, Phaseolus, potato, Pseuderanthemum, pumpkin, Rhynchosia, rice, Serrano, Sida, sorghum, soybean, squash, sugarcane, sugarbeet, sunflower, sweet potato, tea, tomato, tobacco, watermelon, wheat and Wissadula.

17. The method of claim 1 wherein said ssDNA virus is a
25 Geminivirus family virus.

18. The method of claim 17 wherein said Geminivirus is selected from the group consisting of Mastrevirus, Curtovirus and Begomovirus genera.

19. The method of claim 1 wherein said ssDNA virus is a
30 Mastrevirus genus species selected from the group consisting of Bajra streak virus, Bean yellow dwarf virus, Bromus striate mosaic virus, Chickpea chlorotic dwarf virus, Chloris striate

mosaic virus, Digitaria streak virus, Digitaria striate mosaic virus, Maize streak virus//Ethiopia, Maize streak virus//Ghana1, Maize streak virus//Ghana2, Maize streak virus//Kenya, Maize streak virus//Komatipoort, Maize streak virus//Malawi, Maize streak virus//Mauritius, Maize streak virus//Mozambique, Maize streak virus//Nigeria1, Maize streak virus//Nigeria2, Maize streak virus//Nigeria3, Maize streak virus//Port Elizabeth, Maize streak virus//Reunion1, Maize streak virus//Reunion2, Maize streak virus//Setaria, Maize streak virus//South Africa, Maize streak virus//Tas, Maize streak virus//Uganda, Maize streak virus//Vaalhart maize, Maize streak virus//Vaalhart wheat, Maize streak virus//Wheat-eleusian, Maize streak virus//Zaire, Maize streak virus//Zimbabwe1, Maize streak virus//Zimbabwe2, Miscanthus streak virus, Panicum streak virus/Karino, Panicum streak virus/Kenya, Paspalum striate mosaic virus, Sugarcane streak virus//Egypt, Sugarcane streak virus/Natal, Sugarcane streak virus/Mauritius, Tobacco yellow dwarf virus, Wheat dwarf virus/Czech Republic [Wheat dwarf virus-CJI, WDV-CJI], Wheat dwarf virus/France and Wheat dwarf virus/Sweden.

20. The method of claim 1 wherein said ssDNA virus is a Curtovirus genus species selected from the group consisting of Beet curly top virus-California, Beet curly top virus-California//Logan, Beet curly top virus-CFH, Beet curly top virus//Iran, Beet curly top virus-Worland, Horseradish curly top virus, Tomato leafroll virus and Tomato pseudo-curly top virus.

21. The method of claim 1 wherein said ssDNA virus is a Begomovirus genus species selected from the group consisting of Abutilon mosaic virus, Acalypha yellow mosaic virus, African cassava mosaic virus//Ghana, African cassava mosaic virus/Kenya, African cassava mosaic virus/Nigeria, African cassava mosaic

virus/Uganda, Ageratum yellow vein virus, Althea rosea enation virus, Asystasia golden mosaic virus, Bean calico mosaic virus, Bean dwarf mosaic virus, Bean golden mosaic virus-Brazil, Bean golden mosaic virus-Puerto Rico, Bean golden mosaic virus-Puerto Rico/Dominican Rep. [Bean golden mosaic virus-Dominican Rep., BGMV-DR], Bean golden mosaic virus-Puerto Rico/Guatemala [Bean golden mosaic virus-Guatemala, BGMV-GA], Bhendi yellow vein mosaic virus, Chino del tomate virus [Tomato leaf crumple virus, TLCrV], Cotton leaf crumple virus, Cotton leaf curl virus-India, Cotton leaf curl virus-Pakistan1/Faisalabad1 [Cotton leaf curl virus-Pakistan2], Cotton leaf curl virus-Pakistan1/Faisalabad2 [Cotton leaf curl virus-Pakistan3], Cotton leaf curl virus-Pakistan1/Multan [Cotton leaf curl virus-Pakistan1], Cotton leaf curl virus-Pakistan2/Faisalabad [Pakistani cotton leaf curl virus], Cowpea golden mosaic virus, Croton yellow vein mosaic virus//Lucknow, Dolichos yellow mosaic virus, East african cassava mosaic virus/Kenya, East african cassava mosaic virus/Malawi, East african cassava mosaic virus/Tanzania, East african cassava mosaic virus/Uganda//1 [African cassava mosaic virus-Uganda variant], East african cassava mosaic virus/Uganda//2, Eclipta yellow vein virus, Eggplant yellow mosaic virus, Eupatorium yellow vein virus, Euphorbia mosaic virus, Honeysuckle yellow vein mosaic virus, Horsegram yellow mosaic virus, Indian cassava mosaic virus, Jatropha mosaic virus, Leonurus mosaic virus, Limabean golden mosaic virus, Lupin leaf curl virus, Macroptilium golden mosaic virus-Jamaica//2, Macroptilium golden mosaic virus-Jamaica//3, Macrotyloma mosaic virus, Malvaceous chlorosis virus, Melon leaf curl virus, Mungbean yellow mosaic virus, Okra leaf curl virus//Ivory Coast, Okra leaf curl virus//India, Papaya leaf curl virus, Pepper huasteco virus,

Pepper golden mosaic virus, [Texas pepper virus], Pepper mild tigrÃ virus, Potato yellow mosaic virus//Guadeloupe, Potato yellow mosaic virus/Trinidad and Tobago, Potato yellow mosaic virus/Venezuela, Pseuderanthemum yellow vein virus,

5 Rhynchosia mosaic virus, Serrano golden mosaic virus, Sida golden mosaic virus/Costa Rica, Sida golden mosaic virus/Honduras, Sida golden mosaic virus/Honduras//Yellow vein, Sida yellow vein virus, Solanum apical leaf curl virus, Soybean crinkle leaf virus, Squash leaf curl virus, Squash leaf curl

10 virus/Extended host, Squash leaf curl virus/Restricted host, Squash leaf curl virus/Los Mochis, Squash leaf curl virus-China, Tomato golden mosaic virus/Common strain, Tomato golden mosaic virus/Yellow vein strain, Tobacco leaf curl virus//India, Tobacco leaf curl virus-China, Tomato

15 leaf curl virus//Solanum species D1, Tomato leaf curl virus//Solanum species D2, Tomato leaf curl virus-Australia, Tomato leaf curl virus-Bangalore1 [Indian tomato leaf curl virus-BangaloreI], Tomato leaf curl virus-Bangalore2, [Indian tomato leaf curl virus, ItoLCV], Tomato leaf curl

20 virus-Bangalore3 [Indian tomato leaf curl virus- BangaloreII], Tomato leaf curl virus-New Delhi/Severe [Tomato leaf curl virus-India2, ToLCV-IN1], Tomato leaf curl virus-New Delhi/Mild [Tomato leaf curl virus-India2, ToLCV-IN2], Tomato leaf curl virus-New Delhi/Lucknow [Indian tomato leaf curl virus], Tomato

25 leaf curl virus//Senegal, Tomato leaf curl virus-Sinaloa [Sinaloa tomato leaf curl virus, STL CV], Tomato leaf curl virus-Taiwan, Tomato leaf curl virus-Tanzania, Tomato mottle virus, Tomato mottle virus-Taino [Taino tomato mottle virus, TTMOV], Tomato severe leaf curl virus//Guatemala, Tomato severe

30 leaf curl virus//Honduras, Tomato severe leaf curl virus//Nicaragua, Tomato yellow dwarf virus, Tomato yellow leaf curl virus-China, Tomato yellow leaf curl virus-Israel, Tomato

yellow leaf curl virus-Israel/Mild, Tomato yellow leaf curl virus-Israel/Egypt, [Tomato yellow leaf curl virus-Egypt, TYLCV-EG], Tomato yellow leaf curl virus-Israel//Cuba, Tomato yellow leaf curl virus-Israel//Jamaica, Tomato yellow leaf curl virus-Israel//Saudi Arabia¹, [Tomato yellow leaf curl virus-Northern Saudi Arabia, TYLCV-NSA], Tomato yellow leaf curl virus-Nigeria, Tomato yellow leaf curl virus-Sardinia, Tomato yellow leaf curl virus-Sardinia/Sicily [Tomato yellow leaf curl virus-Sicily, TYLCV-SY], Tomato yellow leaf curl virus-Sardinia/Spain//1 [Tomato yellow leaf curl virus-Spain, TYLCV-Sp], Tomato yellow leaf curl virus-Sardinia/Spain//2 [Tomato yellow leaf curl virus-Almeria, TYLCV-Almeria], Tomato yellow leaf curl virus-Sardinia/Spain//3 [Tomato yellow leaf curl virus-European strain], Tomato yellow leaf curl virus-Saudi Arabia [Tomato yellow leaf curl virus-Southern Saudi Arabia, TYLCV-SSA], Tomato yellow leaf curl virus-Tanzania, Tomato yellow leaf curl virus-Thailand//1, Tomato yellow leaf curl virus-Thailand//2, Tomato yellow leaf curl virus//Yemen, Tomato yellow mosaic virus-Brazil//1, Tomato yellow mosaic virus-Brazil//2, Tomato yellow mottle virus, Tomato yellow vein streak virus-Brazil, Watermelon chlorotic stunt virus, Watermelon curly mottle virus and Wissadula golden mosaic virus-Jamaica//1.

22. The method of claim 1 wherein said ssDNA virus is Banana bunchy top virus, Coconut foliar decay virus, Fababean necrotic yellows virus, Milk vetch dwarf virus or Subterranean clover stunt virus.

23. The method of claim 1 wherein said ssDNA virus is geminivirus and said ssDNA-binding protein is Coliphage M13 gene 5 protein.

24. A method for producing geminivirus resistance in a plant comprising introducing into said plant a gene capable of

expressing Coliphage M13 gene 5 protein in said plant.

25. A DNA expression vector comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family, wherein said vector is capable of expressing said
5 protein in plants.

26. The DNA expression vector of claim 25 wherein said Inoviridae family virus is selected from the group consisting of the Inovirus and Plectrovirus genuses.

27. The DNA expression vector of claim 26 wherein said
10 Inovirus genus virus is selected from the group consisting of Coliphage, enterobacteria phage, Pseudomonas phage, Vibrio phage and Xanthomonas phage species.

28. The DNA expression vector of claim 27 wherein said Coliphage species of virus is selected from the group consisting
15 of AE2, dA, Ec9, f1, fd, HR, M13, ZG/2 and ZJ/2 coliphages.

29. The DNA expression vector of claim 25 wherein said ssDNA-binding protein is a coat protein or a gene 5 protein.

30. The DNA expression vector of claim 25 wherein said ssDNA-binding protein is the Coliphage M13 gene 5 protein.

20 31. The DNA expression vector of claim 30 wherein said Coliphage M13 gene 5 protein has the amino acid residue sequence of SEQ ID NO 1.

32. The DNA expression vector of claim 25 wherein said nucleotide sequence comprises a nucleotide sequence shown in SEQ
25 ID NOs 2 or 3.

33. The DNA expression vector of claim 25 wherein said vector is a carrier vector

34. The DNA expression vector of claim 33 wherein said carrier vector is an Agrobacterium vector.

30 35. The DNA expression vector of claim 25 wherein said plant is selected from the group consisting of Abutilon, Acalypha, apple, Ageratum, Althea rosea, Asystasia, Bajra,

banana, barley, beans, beet, Blackgram, Bromus, Cassava, chickpea, Chillies, Chloris, clover, coconut, coffee, cotton, cowpea, Croton, cucumber, Digitaria, Dolichos, eggplant, Eupatorium, Euphorbia, fababean, honeysuckle, horsegram, 5 Jatropha, Leonurus, limabean, Lupin, Macroptilium, Macrotyloma, maize, melon, millet, mungbean, oat, okra, Panicum, papaya, Paspalum, peanut, pea, pepper, pigeon pea, pineapple, Phaseolus, potato, Pseuderanthemum, pumpkin, Rhynchosia, rice, Serrano, Sida, sorghum, soybean, squash, sugarcane, sugarbeet, sunflower, 10 sweet potato, tea, tomato, tobacco, watermelon, wheat and Wissadula.

36. The DNA expression vector of claim 25 wherein said ssDNA virus is a Geminivirus family virus.

37. The DNA expression vector of claim 36 wherein said 15 Geminivirus is selected from the group consisting of Mastrevirus, Curtovirus and Begomovirus genera.

38. The DNA expression vector of claim 25 wherein said ssDNA virus is geminivirus and said ssDNA-binding protein is Coliphage M13 gene 5 protein.

20 39. A composition for producing resistance to a ssDNA virus that infects plants comprising an effective amount of a DNA expression vector comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family, wherein said vector is capable of expressing said protein in 25 said plant.

40. The composition of claim 39 wherein said DNA expression vector is the vector of claim 25.

41. The composition of claim 39 wherein said ssDNA-binding protein is the Coliphage M13 gene 5 protein.

30 42. The composition of claim 39 wherein said Coliphage M13 gene 5 protein has the amino acid residue sequence of SEQ ID NO 1.

43. The composition of claim 39 wherein said nucleotide sequence comprises a nucleotide sequence shown in SEQ ID NOs 2 or 3.

44. The composition of claim 39 wherein said DNA expression vector is a carrier vector.

45. The composition of claim 44 wherein said carrier vector is an Agrobacterium vector.

46. A transgenic plant containing a DNA expression vector comprising a nucleotide sequence that encodes a ssDNA-binding protein of the Inoviridae virus family, wherein said vector is capable of expressing said protein in said plant.

47. The transgenic plant of claim 46 wherein said DNA expression vector is the vector of claim 25.

48. The transgenic plant of claim 46 wherein said ssDNA-binding protein is the Coliphage M13 gene 5 protein.

49. The transgenic plant of claim 48 wherein said Coliphage M13 gene 5 protein has the amino acid residue sequence of SEQ ID NO 1.

50. The transgenic plant of claim 46 wherein said nucleotide sequence comprises a nucleotide sequence shown in SEQ ID NOs 2 or 3.

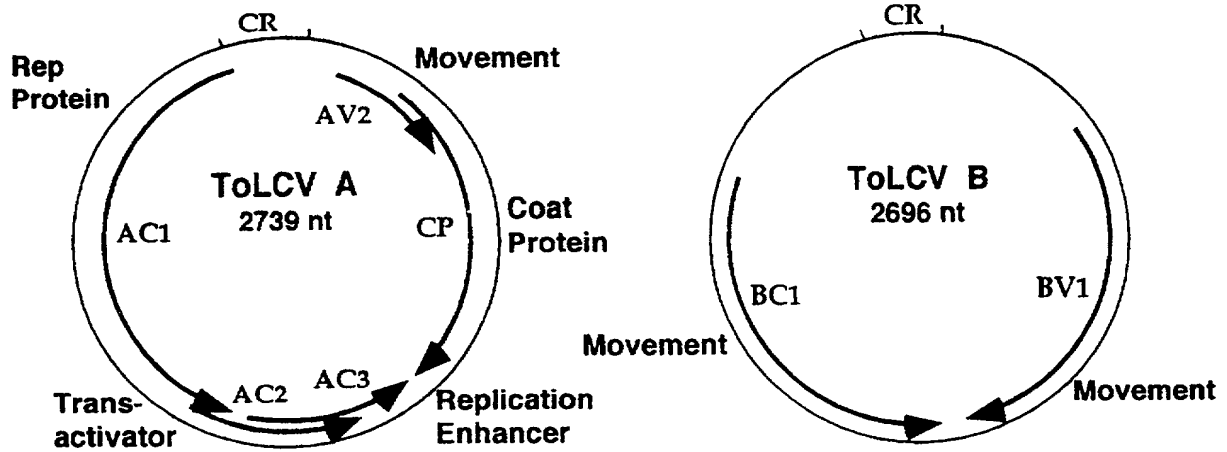


FIG. 1A

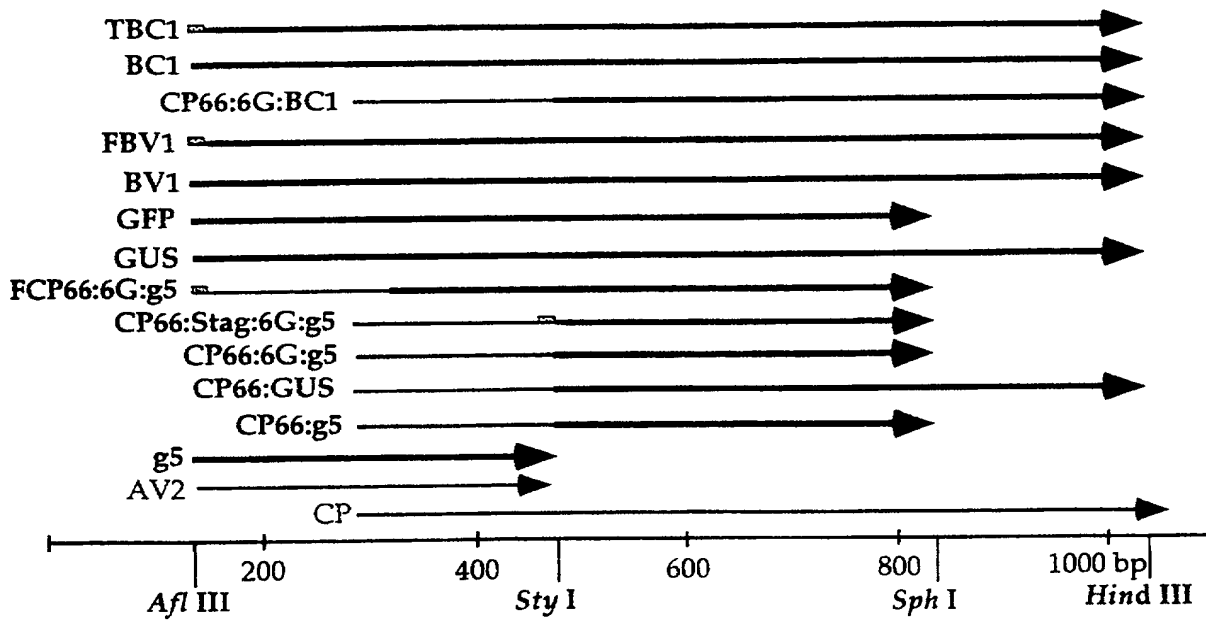


FIG. 1B

2/5

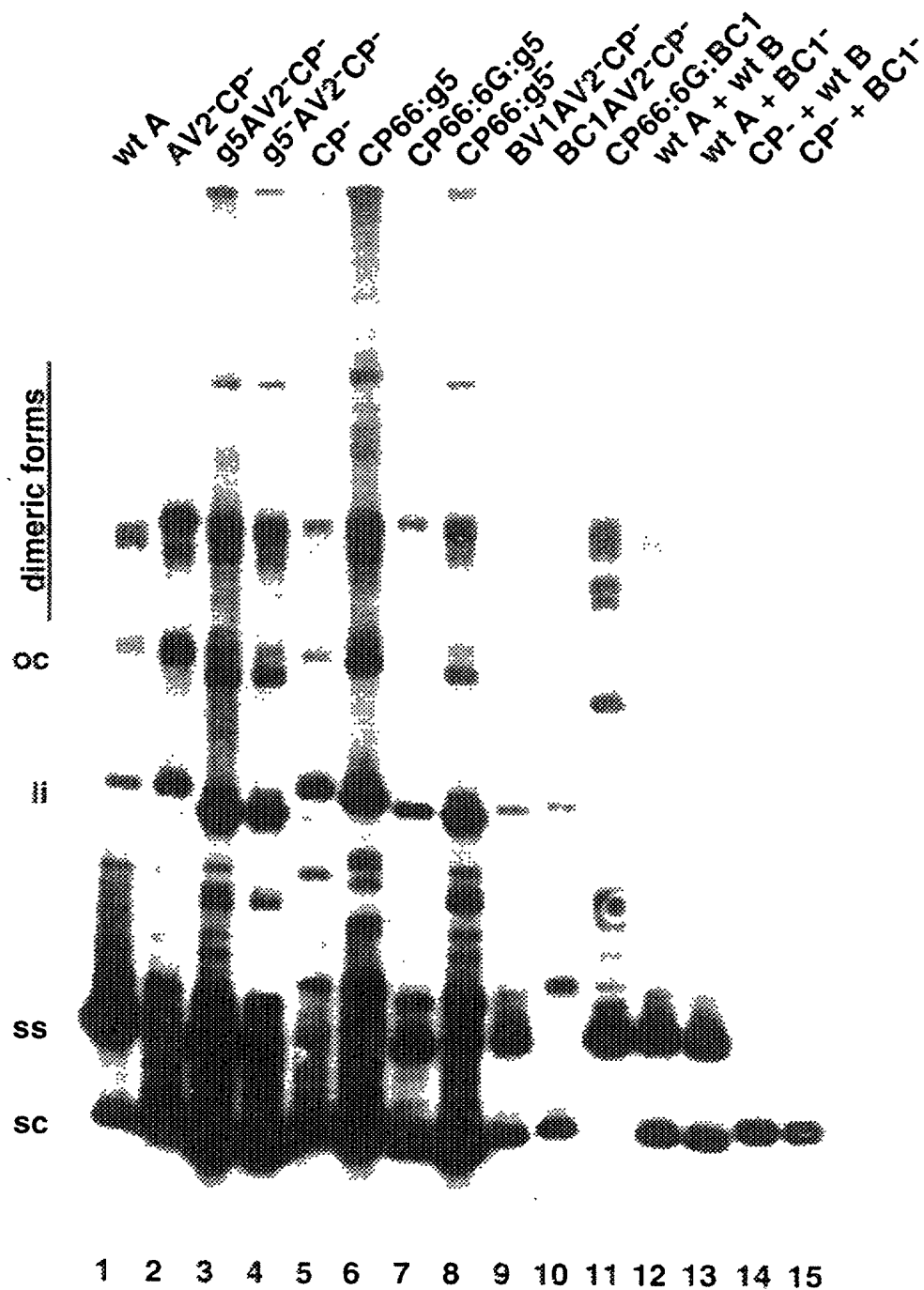


FIG. 2

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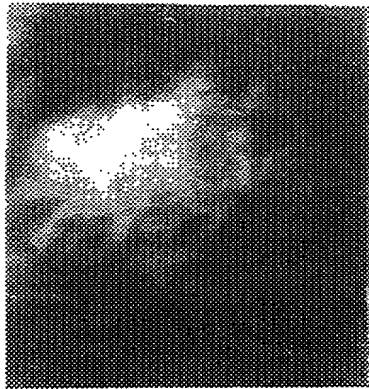


FIG. 3D

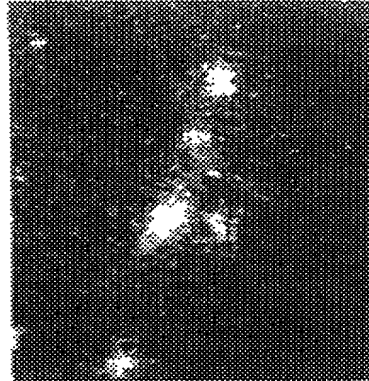


FIG. 3H

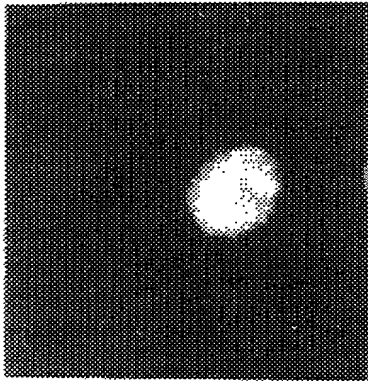


FIG. 3C

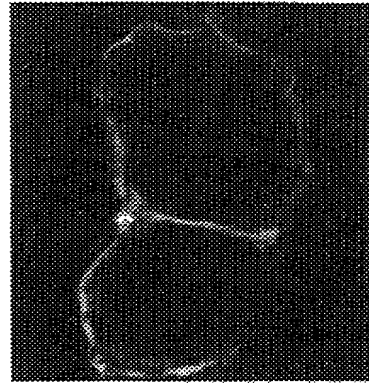


FIG. 3G

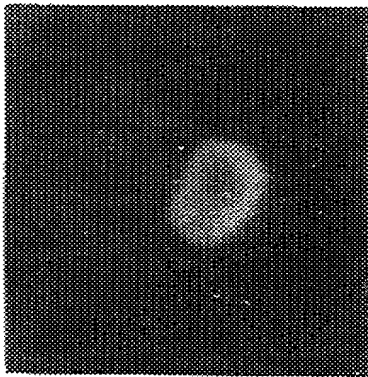


FIG. 3B

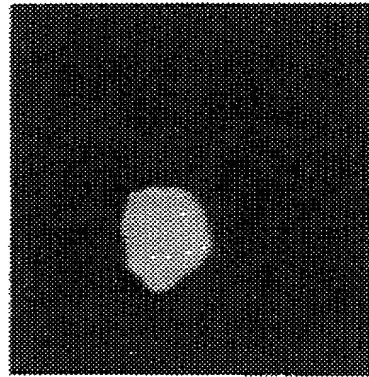


FIG. 3F

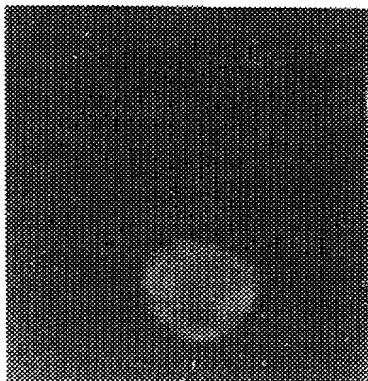


FIG. 3A



FIG. 3E

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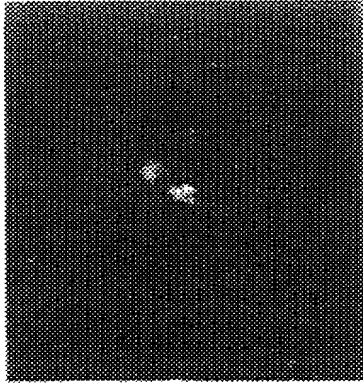


FIG. 3L

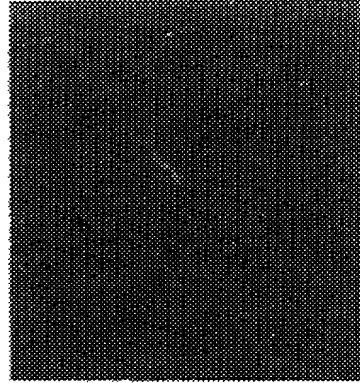


FIG. 3P

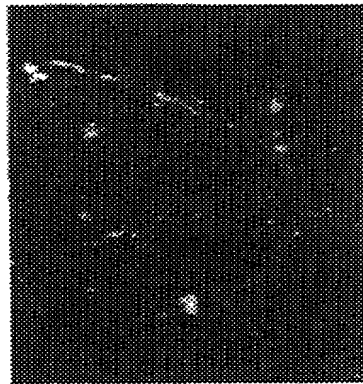


FIG. 3K

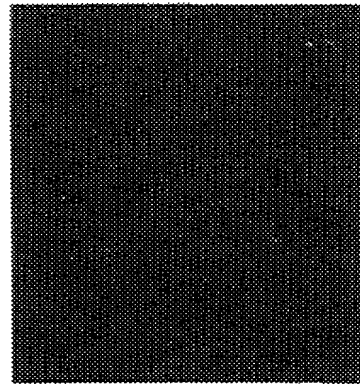


FIG. 3O

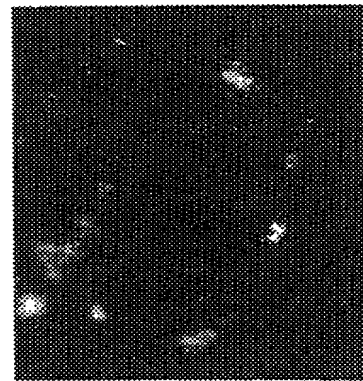


FIG. 3J

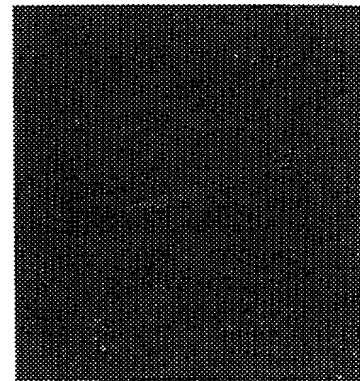


FIG. 3N

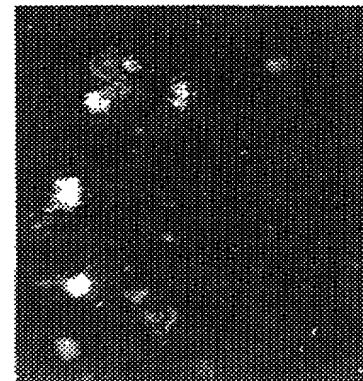


FIG. 3I

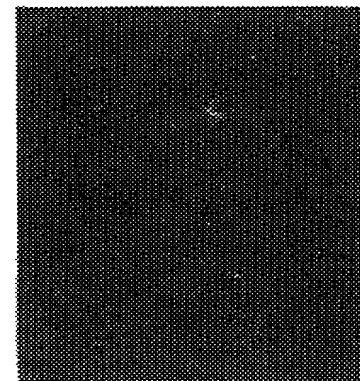


FIG. 3M

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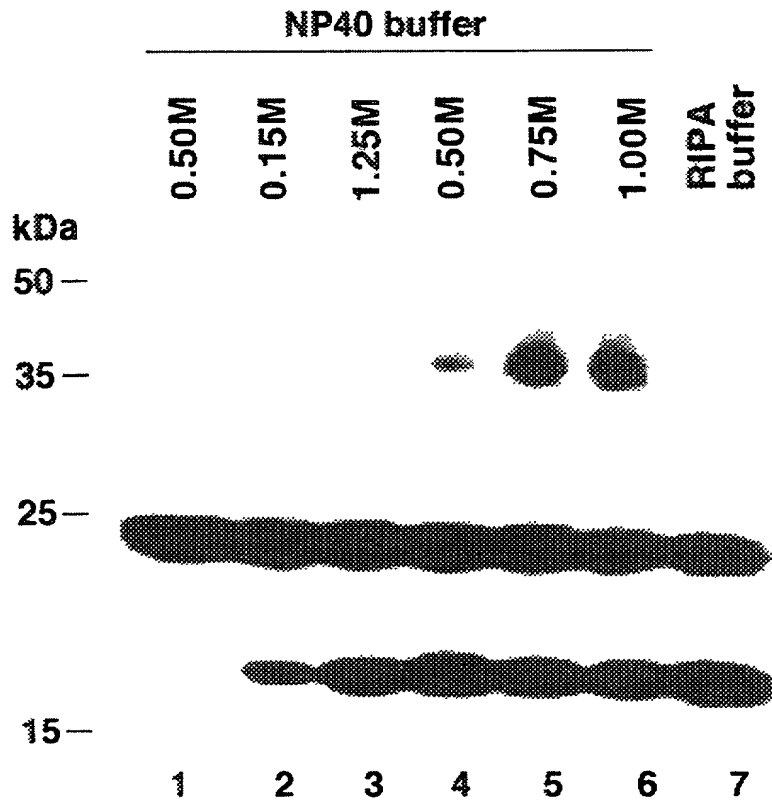


FIG. 4A

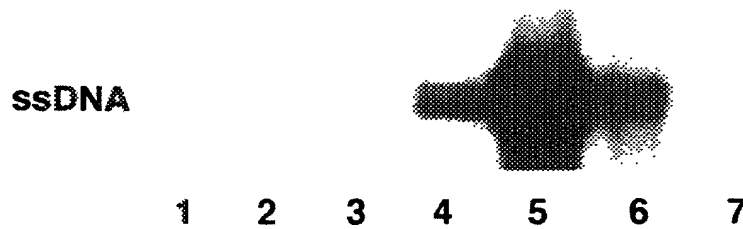


FIG. 4B

PATENT APPLICATION DECLARATION AND POWER OF ATTORNEY

I HEREBY DECLARE THAT:

My residence, post office address, and citizenship are as stated next to my name in PART A of page 2 hereof.

I believe I am the original, first, and sole inventor (if only one name is listed) or an original, first, and joint inventor (if plural names are listed) of the subject matter which is claimed and for which a patent is sought on the invention entitled RESISTANCE IN PLANTS TO INFECTION BY ssDNA VIRUS USING INOVIRIDAE VIRUS ssDNA-BINDING PROTEIN, COMPOSITIONS AND METHODS OF USE the specification of which:

_____ is attached hereto
X was filed on March 3, 1999 as Application Serial No. PCT/US99/04716
and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Sec. 1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, Sec. 119 of any foreign application(s) for patent or inventor's certificate listed in PART B on page 2 hereof and have also identified in PART B on page 2 hereof any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

I hereby claim the benefit under Title 35, United States Code, Sec. 120 of any United States application(s) listed in PART C on page 2 hereof and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, Sec. 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Sec. 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I hereby appoint the following as my attorneys or agents with full power of substitution to prosecute this application and transact all business in the United States Patent and Trademark Office connected therewith:

<u>5</u> Douglas A. Bingham	Reg. No. <u>32,457</u>	Emily Holmes	Reg. No. <u>40,652</u>
Thomas Fitting	Reg. No. <u>34,163</u>	Thomas E. Northrup	Reg. No. <u>33,268</u>
Donald G. Lewis	Reg. No. <u>28,636</u>		

whose mailing address for this application is:

THE SCRIPPS RESEARCH INSTITUTE
10550 North Torrey Pines Road, Mail Drop: TPC-8
La Jolla, California 92037

See Page 2 attached, signed, and made a part hereof.

PATENT APPLICATION DECLARATION AND POWER OF ATTORNEY

PART A: Inventor Information And Signature

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Residence (if different) PA

Inventor's Signature: Malla Padidam Date: 4/21/99

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St. Louis, Missouri 63105

Residence (if different) MO

Second Inventor's Signature: Rgn N Beachy Date: 4/26/99

Full name of THIRD joint inventor, if any Claude M. Fauquet
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Del Mar, California 92130

Residence (if different) CA

Third Inventor's Signature: [Signature] Date: 4/26/99

Full name of FOURTH joint inventor, if any _____
Citizenship _____ Post Office Address _____

Residence (if different) _____

Fourth Inventor's Signature: _____ Date: _____

Full name of FIFTH joint inventor, if any _____
Citizenship _____ Post Office Address _____

Residence (if different) _____

Fifth Inventor's Signature: _____ Date: _____

PART B: Prior Foreign Application(s)

Serial No.	Country	Day/Month/Year Filed	Priority Claimed
			<input type="checkbox"/> Yes <input type="checkbox"/> No

PART C: Claim For Benefit of Filing Date of Earlier U.S. Application(s)

Serial No.	Filing Date	Status:
60/076,627	3/3/98	<input type="checkbox"/> Patented <input type="checkbox"/> Pending <input checked="" type="checkbox"/> Abandoned

See Page 1 to which this is attached and from which this Page 2 continues.

SEQUENCE LISTING

SEQ ID NO 1 Amino acid residue sequence of the wild type M13
gene 5 (87 amino acids):

5

MIKVEIKPSQ AQFTTRSGVS RQGKPYSLE QLCYVDLGNE YPVLVKITLD
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10 SEQ ID NO 2 wild type M13 gene 5 nucleic acid sequence

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SEQ ID NO 3 synthetic M13 gene 5 nucleic acid sequence

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SEQ ID NO 4

30 ToLCV New Delhi Component A nucleic acid sequence
GenBank Accession number : U15015

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15 SEQ ID NO 5

ToLCV New Delhi Component B nucleic acid sequence
GenBank Accession number : U15016

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CTTTCGTA 3'

SEQ ID NO 6 pBluescript SK plasmid expression vector

5'

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10 TTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCAT
CCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCG
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GATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAG
15 CGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGG
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TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCGCGCACATT
TCCCCGAAAAGTGC 3'